



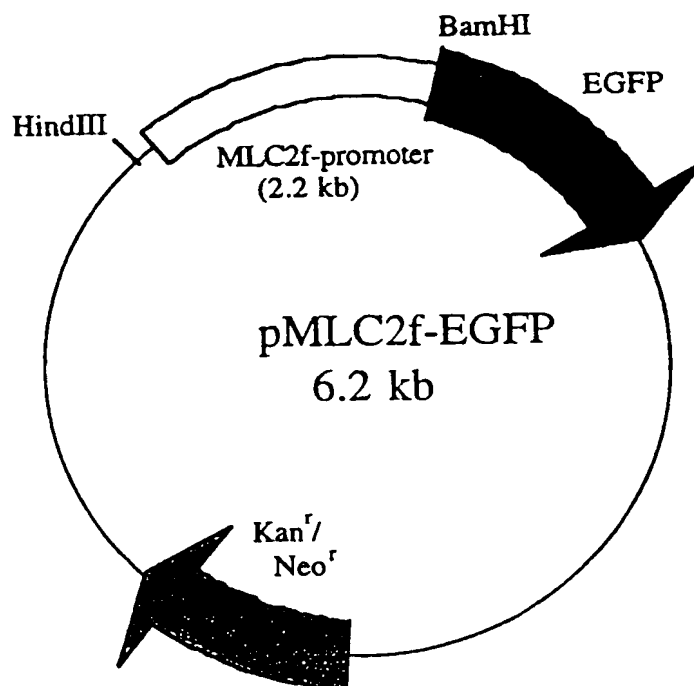
INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/12, 5/16, C12Q 1/66, 1/48		A1	(11) International Publication Number: WO 00/49150
			(43) International Publication Date: 24 August 2000 (24.08.00)
(21) International Application Number: PCT/SG99/00079		(74) Agent: APPLIED RESEARCH CORPORATION; Kent Ridge, P.O. Box 1016, Singapore 911101 (SG).	
(22) International Filing Date: 16 July 1999 (16.07.99)			
(30) Priority Data: 9900811-2 18 February 1999 (18.02.99) SG Not furnished 14 July 1999 (14.07.99) SG		(81) Designated States: CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).	
(71) Applicants (for all designated States except US): NATIONAL UNIVERSITY OF SINGAPORE [SG/SG]; 10 Kent Ridge Crescent, Singapore 119260 (SG). XU, Yianfei [CN/SG]; Intro, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260 (SG). HE, Jiangyan [CN/SG]; Intro, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260 (SG). YAN, Tie [CN/SG]; Intro, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260 (SG).		Published With international search report.	
(72) Inventors; and (75) Inventors/Applicants (for US only): GONG, Zhiyuan [CA/SG]; Intro, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260 (SG). LAM, Toong, Jin [SG/SG]; Intro, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260 (SG). JU, Bensheng [CN/SG]; Intro, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260 (SG).			

(54) Title: CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT TRANSGENIC ORNAMENTAL FISH

(57) Abstract

Four zebrafish gene promoters, which are skin specific, muscle specific, skeletal muscle specific and ubiquitously expressed respectively, were isolated and ligated to the 5' end of the EGFP gene. When the resulting chimeric gene constructs were introduced into zebrafish, the transgenic zebrafish emit green fluorescence under a blue light or ultra-violet light according to the specificity of the promoters used. Thus, new varieties of ornamental fish of different fluorescence patterns, e.g., skin fluorescence, muscle fluorescence, skeletal muscle-specific and/or ubiquitous fluorescence, are developed.



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CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT TRANSGENIC ORNAMENTAL FISH

FIELD OF THE INVENTION

5 This invention relates to fish gene promoters and chimeric gene constructs with these promoters for generation of transgenic fish, particularly fluorescent transgenic ornamental fish.

BACKGROUND OF THE INVENTION

Transgenic technology involves the transfer of a foreign gene into a host organism enabling the host to acquire a new and inheritable trait. The technique was first developed
10 in mice by Gordon et al. (1980). They injected foreign DNA into fertilized eggs and found that some of the mice developed from the injected eggs retained the foreign DNA. Applying the same technique, Palmiter et al. (1982) have introduced a chimeric gene containing a rat growth hormone gene under a mouse heavy metal-inducible gene promoter and generated the first batch of genetically engineered supermice, which are almost twice
15 as large as non-transgenic siblings. This work has opened a promising avenue in using the transgenic approach to provide to animals new and beneficial traits for livestock husbandry and aquaculture.

In addition to the stimulation of somatic growth for increasing the gross production of animal husbandry and aquaculture, transgenic technology also has many other potential
20 applications. First of all, transgenic animals can be used as bioreactors to produce commercially useful compounds by expression of a useful foreign gene in milk or in blood. Many pharmaceutically useful protein factors have been expressed in this way. For example, human α 1-antitrypsin, which is commonly used to treat emphysema, has been expressed at a concentration as high as 35 mg/ml (10% of milk proteins) in the milk of
25 transgenic sheep (Wright et al., 1991). Similarly, the transgenic technique can also be used to improve the nutritional value of milk by selectively increasing the levels of certain valuable proteins such as caseins and by supplementing certain new and useful proteins such as lysozyme for antimicrobial activity (Maga and Murray, 1995). Second, transgenic
30 mice have been widely used in medical research, particularly in the generation of transgenic animal models for human disease studies (Lathe and Mullins, 1993). More recently, it has been proposed to use transgenic pigs as organ donors for xenotransplantation by expressing human regulators of complement activation to prevent hyperacute rejection during organ transplantation (Cozzi and White, 1995). The

development of disease resistant animals has also been tested in transgenic mice (e.g. Chen et al., 1988).

Fish are also an intensive research subject of transgenic studies. There are many ways of introducing a foreign gene into fish, including: microinjection (e.g. Zhu et al., 1985; Du et al., 1992), electroporation (Powers et al., 1992), sperm-mediated gene transfer (Khoo et al., 1992; Sin et al., 1993), gene bombardment or gene gun (Zelegnin et al., 1991), liposome-mediated gene transfer (Szelei et al., 1994), and the direct injection of DNA into muscle tissue (Xu et al., 1999). The first transgenic fish report was published by Zhu et al. (1985) using a chimeric gene construct consisting of a mouse metallothionein gene promoter and a human growth hormone gene. Most of the early transgenic fish studies have concentrated on growth hormone gene transfer with an aim of generating fast growing "superfish". A majority of early attempts used heterologous growth hormone genes and promoters and failed to produce gigantic superfish (e.g. Chourrout et al., 1986; Penman et al., 1990; Brem et al., 1988; Gross et al., 1992). But enhanced growth of transgenic fish has been demonstrated in several fish species including Atlantic salmon, several species of Pacific salmon, and loach (e.g. Du et al., 1992; Delvin et al., 1994, 1995; Tsai et al., 1995).

The zebrafish, *Danio rerio*, is a new model organism for vertebrate developmental biology. As an experimental model, the zebrafish offers several major advantages such as easy availability of eggs and embryos, tissue clarity throughout embryogenesis, external development, short generation time and easy maintenance of both the adult and the young. Transgenic zebrafish have been used as an experimental tool in zebrafish developmental biology. However, despite the fact that the first transgenic zebrafish was reported a decade ago (Stuart et al., 1988), most transgenic zebrafish work conducted so far used heterologous gene promoters or viral gene promoters: e.g. viral promoters from SV40 (simian virus 40) and RSV (Rous sarcoma virus) (Stuart et al., 1988, 1990; Bayer and Campos-Ortega, 1992), a carp actin promoter (Liu et al., 1990), and mouse homeobox gene promoters (Westerfield et al., 1992). As a result, the expression pattern of a transgene in many cases is variable and unpredictable.

GFP (green fluorescent protein) was isolated from a jelly fish, *Aequorea victoria*. The wild type GFP emits green fluorescence at a wavelength of 508 nm upon stimulation with ultraviolet light (395 nm). The primary structure of GFP has been elucidated by cloning of its cDNA and genomic DNA (Prasher et al., 1992). A modified GFP, also called EGFP (Enhanced Green Fluorescent Protein) has been generated artificially and it contains mutations that allow the protein to emit a stronger green light and its coding sequence has also been optimized for higher expression in mammalian cells based on preferable human

codons. As a result, EGFP fluorescence is about 40 times stronger than the wild type GFP in mammalian cells (Yang et al., 1996). GFP (including EGFP) has become a popular tool in cell biology and transgenic research. By fusing GFP with a tested protein, the GFP fusion-protein can be used as an indicator of the subcellular location of the tested protein
5 (Wang and Hazelrigg, 1994). By transformation of cells with a functional GFP gene, the GFP can be used as a marker to identify expressing cells (Chalfie et al., 1994). Thus, the GFP gene has become an increasingly popular reporter gene for transgenic research as GFP can be easily detected by a non-invasive approach.

The GFP gene (including EGFP gene) has also been introduced into zebrafish in
10 several previous reports by using various gene promoters, including *Xenopus elongation factor 1 α* enhancer-promoter (Amsterdam et al., 1995, 1996), rat *myosin light-chain* enhancer (Moss et al., 1996), zebrafish *GATA-1* and *GATA-3* promoters (Meng et al., 1997; Long et al., 1997), zebrafish α - and β -*actin* promoters (Higashijima et al., 1997), and tilapia *insulin-like growth factor I* promoter (Chen et al., 1998). All of these transgenic
15 experiments aim at either developing a GFP transgenic system for gene expression analysis or at testing regulatory DNA elements in gene promoters.

SUMMARY OF THE INVENTION

It is a primary objective of the invention to clone fish gene promoters that are constitutive (ubiquitous), or that have tissue specificity such as skin specificity or muscle
20 specificity or that are inducible by a chemical substance, and to use these promoters to develop effective gene constructs for production of transgenic fish.

It is another objective of the invention to develop fluorescent transgenic ornamental fish using these gene constructs. By applying different gene promoters, tissue-specific, inducible under different environmental conditions, or ubiquitous, to drive the GFP gene,
25 GFP could be expressed in different tissues or ubiquitously. Thus, these transgenic fish may be skin fluorescent, muscle fluorescent, ubiquitously fluorescent, or inducibly fluorescent. These transgenic fish may be used for ornamental purposes, for monitoring environmental pollution, and for basic studies such as recapitulation of gene expression programs or monitoring cell lineage and cell migration. These transgenic fish may be used
30 for cell transplantation and nuclear transplantation or fish cloning.

Other objectives, features and advantages of the present invention will become apparent from the detailed description which follows, or may be learned by practice of the invention.

Four zebrafish gene promoters of different characteristics were isolated and four chimeric gene constructs containing a zebrafish gene promoter and EGFP DNA were made: pCK-EGFP, pMCK-EGFP, pMLC2f-EGFP and pARP-EGFP. The first chimeric gene-construct, pCK-EGFP, contains a 2.2 kbp polynucleotide comprising a zebrafish
5 cytokeratin (CK) gene promoter which is specifically or predominantly expressed in skin epithelia. The second one, pMCK-EGFP, contains a 1.5 kbp polynucleotide comprising a muscle-specific promoter from a zebrafish muscle creatine kinase (MCK) gene and the gene is only expressed in the muscle tissue. The third construct, pMLC2f-EGFP contains a
10 2.2 kbp polynucleotide comprising a strong skeletal muscle-specific promoter from the fast skeletal muscle isoform of the myosin light chain 2 (MLC2f) gene and is expressed specifically or predominantly in skeletal muscle. The fourth chimeric gene construct, pARP-EGFP, contains a strong and ubiquitously expressed promoter from a zebrafish acidic ribosomal protein (ARP) gene. These four chimeric gene constructs have been
15 introduced into zebrafish at the one cell stage or two cell stage by microinjection. In all cases, the GFP expression patterns were consistent with the specificities of the promoters. GFP was predominantly expressed in skin epithelia with pCK-EGFP, specifically expressed in muscles with pMCK-EGFP, specifically expressed in skeletal muscles with pMLC2f-EGFP and ubiquitously expressed in all tissues with pARP-EGFP.

These chimeric gene constructs are useful to generate green fluorescent transgenic
20 fish. The GFP transgenic fish emit green fluorescence light under a blue or ultraviolet light and this feature makes the genetically engineered fish unique and attractive in the ornamental fish market. The fluorescent transgenic fish are also useful for the development of a biosensor system and as research models for embryonic studies such as cell lineage, cell migration, cell and nuclear transplantation etc.

25 BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A-II are photographs showing expression of CK (Figs. 1A-1C), MCK (Figs. 1D-1E), ARP (Figs. 1F-1G) and MLC2f (Figs. 1H-1I) mRNAs in zebrafish embryos as revealed by whole mount *in situ* hybridization (detailed description of the procedure can be found in Thisse et al., 1993). (Fig. 1A) A 28 hpf (hour postfertilization) embryo hybridized
30 with a CK antisense riboprobe. (Fig. 1B) Enlargement of the mid-part of the embryo shown in Fig. 1A. (Fig. 1C) Cross-section of the embryo in Fig. 1A. (Fig. 1D) A 30 hpf embryo hybridized with an MCK antisense riboprobe. (Fig. 1E) Cross-section of the embryo in Fig 1D. (Fig. 1F) A 28 hpf embryo hybridized with an ARP antisense riboprobe. (Fig. 1G) Cross-section of the embryo in Fig. 1F. Arrows indicate the planes for cross-
35 sections and the box in panel A indicates the enlarged region shown in panel B. (Fig. 1H) Side view of a 22-hpf embryo hybridized with the MLC2f probe. (Fig. 1I) Transverse

section through the trunk of a stained 24-hpf embryo. SC, spinal cord; N, notochord.

Fig. 2A is a digitized image showing distribution of CK, MCK and ARP mRNAs in adult tissues. Total RNAs were prepared from selected adult tissues as indicated at the top of each lane and analyzed by Northern blot hybridization (detailed description of the procedure can be found in Gong et al., 1992). Three identical blots were made from the same set of RNAs and hybridized with the CK, MCK and ARP probes, respectively.

Fig. 2B is a digitized image showing distribution of MLC2f mRNA in adult tissues. Total RNAs were prepared from selected adult tissues as indicated at the top of each lane and analyzed by Northern blot hybridization (detailed description of the procedure can be found in Gong et al., 1992). Two identical blots were made from the same set of RNAs and hybridized with the MLC2f probe and a ubiquitously expressed α -actin probe, respectively.

Fig. 3. is a schematic representation of the strategy of promoter cloning. Restriction enzyme digested genomic DNA was ligated with a short linker DNA which consists of Oligo 1 and Oligo 2. Nested PCR reactions were then performed: the first round PCR used linker specific primer L1 and gene specific primers G1, where G1 is CK1, MCK1, M1 or ARP1 in the described embodiments, and the second round linker specific primer L2 and gene specific primer G2, where G2 is CK2, MCK2, M2 or ARP2, respectively in the described embodiments.

Fig. 4 is a schematic map of the chimeric gene construct, pCK-EGFP. The 2.2 kb zebrafish DNA fragment comprising the CK promoter region is inserted into pEGFP-1 (Clontech) at the EcoRI and BamHI site as indicated. In the resulting chimeric DNA construct, the EGFP gene is under control of the zebrafish CK promoter. Also shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pCK-EGFP is 6.4 kb.

Fig. 5 is a schematic map of the chimeric gene construct, pMCK-EGFP. The 1.5 kb zebrafish DNA fragment comprising the MCK promoter region is inserted into pEGFP-1 (Clontech) at the EcoRI and BamHI site as indicated. In the resulting chimeric DNA construct, the EGFP gene is under control of the zebrafish MCK promoter. Also shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pMCK-EGFP is 5.7 kb.

Fig. 6 is a schematic map of the chimeric gene construct, pARP-EGFP. The 2.2 kb zebrafish DNA fragment comprising the ARP promoter/1st intron region is inserted into pEGFP-1 (Clontech) at the EcoRI and BamHI site as indicated. In the resulting chimeric

DNA construct, the EGFP gene is under control of the zebrafish ARP promoter. Also shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pARP-EGFP is 6.4 kb. —

5 Fig. 7 is a schematic map of the chimeric gene construct, pMLC2f-EGFP. The 2.0 kb zebrafish DNA fragment comprising the MLC2f promoter region is inserted into pEGFP-1 (Clontech) at the HindIII and BamHI site as indicated. In the resulting chimeric DNA construct, the EGFP gene is under control of the zebrafish MLC2f promoter. Also
10 shown is the kanamycin/neomycin resistance gene (Kan^r/Neo^r) in the backbone of the original pEGFP-1 plasmid. The total length of the recombinant plasmid pMLC2f-EGFP is 6.2 kb.

Fig. 8 is a photograph of a typical transgenic zebrafish fry (4 days old) with pCK-EGFP, which emits green fluorescence from skin epithelia under a blue light.

15 Fig. 9 is a photograph of a typical transgenic zebrafish fry (3 days old) with pMCK-EGFP, which emits green fluorescence from skeletal muscles under a blue light.

Fig. 10 is a photograph of a typical transgenic zebrafish fry (2 days old) with pARP-EGFP, which emits green fluorescence under a blue light from a variety of cell types such as skin epithelia, muscle cells, lens, neural tissues, notochord, circulating blood cells and yolk cells.

Figs. 11A-11B. Photographs of a typical transgenic zebrafish founder with pMLC2f-EGFP (Fig. 11A) and an F1 stable transgenic offspring (Fig. 11B). Both pictures were taken under an ultraviolet light (365 nm). The green fluorescence can be better observed under a blue light with an optimal wavelength of 488 nm.

Figs. 12A-12C. Examples of high, moderate and low expression of GFP in transiently transgenic embryos at 72 hpf. (Fig. 12A) High expression, GFP expression was detected in essentially 100% of the muscle fibers in the trunk. (Fig. 12B) Moderate expression, GFP expression was detected in several bundles of muscle fibers, usually in the mid-trunk region. (Fig. 12C) Low expression, GFP expression occurred in dispersed muscle fibers and the number of GFP positive fibers is usually less than 20 per embryo.

Fig. 13. Deletion analysis of the MLC2f promoter in transient transgenic zebrafish embryos. A series of 5' deletions of MLC2f-EGFP constructs containing -2011-bp (2-kb), -1338-bp, -873-bp, -283-bp, -77-bp and -3-bp of the MLC2f promoter were generated by unidirectional deletion using the double-stranded Nested Deletion Kit from Pharmacia

based on the manufacturer's instructional manual. Each construct was injected into approximately 100 embryos and GFP expression was monitored in the first 72 hours of embryonic development. The level of GFP expression was classified based on the examples shown in Figs. 12A-12C. Potential E-boxes and MEF2 binding sites, which are important for muscle-specific transcription (Schwarz et al., 1993; Olson et al., 1995), are indicated on the -2011-bp construct.

DETAILED DESCRIPTION OF THE INVENTION

Gene Constructs

To develop successful transgenic fish with a predictable pattern of transgene expression, the first step is to make a gene construct suitable for transgenic studies. The gene construct generally comprises three portions: a gene promoter, a structural gene and transcriptional termination signals. The gene promoter would determine where, when and under what conditions the structural gene is turned on. The structural gene contains protein coding portions that determine the protein to be synthesized and thus the biological function. The structural gene might also contain intron sequences which can affect mRNA stability or which might contain transcription regulatory elements. The transcription termination signals consist of two parts: a polyadenylation signal and a transcriptional termination signal after the polyadenylation signal. Both are important to terminate the transcription of the gene. Among the three portions, selection of a promoter is very important for successful transgenic study, and it is preferable to use a homologous promoter (homologous to the host fish) to ensure accurate gene activation in the transgenic host.

A promoter drives expression "predominantly" in a tissue if expression is at least 2-fold, preferably at least 5-fold higher in that tissue compared to a reference tissue. A promoter drives expression "specifically" in a tissue if the level of expression is at least 5-fold, preferably at least 10-fold higher, more preferably at least 50-fold higher in that tissue than in any other tissue.

Recombinant DNA Constructs

Recombinant DNA constructs comprising one or more of the DNA or RNA sequences described herein and an additional DNA and/or RNA sequence are also included within the scope of this invention. These recombinant DNA constructs usually have sequences which do not occur in nature or exist in a form that does not occur in nature or exist in association with other materials that do not occur in nature. The DNA and/or RNA sequences described as constructs or in vectors above are "operably linked" with other

DNA and/or RNA sequences. DNA regions are operably linked when they are functionally related to each other. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as part of a preprotein which participates in the secretion of the polypeptide; a promoter is operably linked to a coding sequence if it controls the transcription of the coding sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation. Generally, operably linked means contiguous (or in close proximity to) and, in the case of secretory leaders, contiguous and in reading phase.

The sequences of some of the DNAs, and the corresponding proteins encoded by the DNA, which are useful in the invention are set forth in the attached Sequence Listing.

The complete cytokeratin (CK) cDNA sequence is shown in SEQ ID NO:1, and its deduced amino acid sequence is shown in SEQ ID NO:2. The binding sites of the gene specific primers for promoter amplification, CK1 and CK2, are indicated. The extra nucleotides introduced into CK2 for generation of a restriction site are shown as a misc_feature in the primer sequence SEQ ID NO:11. A potential polyadenylation signal, AATAAA, is indicated in SEQ ID NO:1.

The complete muscle creatine kinase (MCK) cDNA sequence is shown in SEQ ID NO:3, and its deduced amino acid sequence is shown in SEQ ID NO:4. The binding sites of the gene specific primers for promoter amplification, MCK1 and MCK2, are indicated. The extra nucleotides introduced into MCK1 and MCK2 for generation of restriction sites are shown as a misc_feature in the primer sequences SEQ ID NOS:12 and 13, respectively. A potential polyadenylation signal, AATAAA, is indicated in SEQ ID NO:3.

The complete fast skeletal muscle isoform of myosin light chain 2 (MLC2f) cDNA sequence is shown in SEQ ID NO:20, and its deduced amino acid sequence is shown in SEQ ID NO:21. The binding sites of the gene-specific primers for promoter amplification, M1 and M2, are indicated. Two potential polyadenylation signals, AATAAA, are shown as a misc_feature in SEQ ID NO:20.

The complete acidic ribosomal protein P0 (ARP) cDNA sequence is shown in SEQ ID NO:5, and its deduced amino acid sequence is shown in SEQ ID NO:6. The binding sites of the gene specific primers for promoter amplification, ARP1 and ARP2, are indicated. The extra nucleotides introduced into ARP2 for generation of a restriction site are shown as a misc_feature in the primer sequence SEQ ID NO:15. A potential polyadenylation signal, AATAAA, is indicated in SEQ ID NO:5.

SEQ ID NO:7 shows the complete sequence of the CK promoter region. A putative

TATA box is shown, and the 3' nucleotides identical to the 5' CK cDNA sequence are shown as a misc_feature. The binding site of the second gene specific primer, CK2, is shown. The introduced BamHI site is indicated as a misc_feature in the primer sequence SEQ ID NO:11.

5 SEQ ID NO:8 shows the complete sequence of the MCK promoter region. A putative TATA box is shown, and the 3' nucleotides identical to the 5' MCK cDNA sequence are shown as a misc_feature in SEQ ID NO:8. The binding site of the second gene specific primer, MCK2, is shown. The introduced BamHI site is indicated as a misc_feature in the primer sequence SEQ ID NO:13.

10 SEQ ID NO:22 shows the complete sequence of the MLC2f promoter region. A putative TATA box is shown, and the 3' nucleotides identical to the 5' MLC2f cDNA sequence are shown as a misc_feature. The binding site of the second gene-specific primer, M2, is shown. Potential muscle-specific cis-elements, E-boxes and MEF2 binding sites, are also shown. The proximal 1-kb region of the MLC2f promoter was recently published (Xu
15 et al., 1999).

 SEQ ID NO:9 shows the complete sequence of the ARP promoter region including the first intron. The first intron is shown, and the 3' nucleotides identical to the 5' ARP cDNA sequence are shown as misc_features. No typical TATA box is found. The binding site of the second gene specific primer, ARP2, is shown. The introduced BamHI site is
20 indicated as a misc_feature in the primer sequence SEQ ID NO:15.

Specifically Exemplified Polypeptides/DNA

 The present invention contemplates use of DNA that codes for various polypeptides and other types of DNA to prepare the gene constructs of the present invention. DNA that codes for structural proteins, such as fluorescent peptides including GFP, EGFP, BFP,
25 EBFP, YFP, EYFP, CFP, ECFP and enzymes (such as luciferase, β -galactosidase, chloramphenicol acetyltransferase, etc.), and hormones (such as growth hormone etc.), are useful in the present invention. More particularly, the DNA may code for polypeptides comprising the sequences exemplified in SEQ ID NOS:2, 4, 6 and 21. The present invention also contemplates use of particular DNA sequences, including regulatory
30 sequences, such as promoter sequences shown in SEQ ID NOS: 7, 8, 9 and 22 or portions thereof effective as promoters. Finally, the present invention also contemplates the use of additional DNA sequences, described generally herein or described in the references cited herein, for various purposes.

Chimeric Genes

The present invention also encompasses chimeric genes comprising a promoter described herein operatively linked to a heterologous gene. Thus, a chimeric gene can comprise a promoter of a zebrafish operatively linked to a zebrafish structural gene other than that normally found linked to the promoter in the genome. Alternatively, the promoter can be operatively linked to a gene that is exogenous to a zebrafish, as exemplified by the GFP and other genes specifically exemplified herein. Furthermore, a chimeric gene can comprise an exogenous promoter linked to any structural gene not normally linked to that promoter in the genome of an organism.

10 Variants of Specifically Exemplified Polypeptide

DNA that codes for variants of the specifically exemplified polypeptides are also encompassed by the present invention. Possible variants include allelic variants and corresponding polypeptides from other organisms, particularly other organisms of the same species, genus or family. The variants may have substantially the same characteristics as the natural polypeptides. The variant polypeptide will possess the primary property of concern for the polypeptide. For example, the polypeptide will possess one or more or all of the primary physical (e.g., solubility) and/or biological (e.g., enzymatic activity, physiologic activity or fluorescence excitation or emission spectrum) properties of the reference polypeptide. DNA of the structural genes of the present invention will encode a protein that produces a fluorescent or chemiluminescent light under conditions appropriate to the particular polypeptide in one or more tissues of a fish. Preferred tissues for expression are skin, muscle, eye and bone.

Substitutions, Additions and Deletions

As possible variants of the above specifically exemplified polypeptides, the polypeptide may have additional individual amino acids or amino acid sequences inserted into the polypeptide in the middle thereof and/or at the N-terminal and/or C-terminal ends thereof so long as the polypeptide possesses the desired physical and/or biological characteristics. Likewise, some of the amino acids or amino acid sequences may be deleted from the polypeptide so long as the polypeptide possesses the desired physical and/or biochemical characteristics. Amino acid substitutions may also be made in the sequences so long as the polypeptide possesses the desired physical and biochemical characteristics. DNA coding for these variants can be used to prepare gene constructs of the present invention.

Sequence Identity

The variants of polypeptides or polynucleotides contemplated herein should possess more than 75% sequence identity (sometimes referred to as homology), preferably more than 85% identity, most preferably more than 95% identity, even more preferably
5 more than 98% identity to the naturally occurring and/or specifically exemplified sequences or fragments thereof described herein. To determine this homology, two sequences are aligned so as to obtain a maximum match using gaps and inserts.

Two sequences are said to be "identical" if the sequence of residues is the same when aligned for maximum correspondence as described below. The term
10 "complementary" applies to nucleic acid sequences and is used herein to mean that the sequence is complementary to all or a portion of a reference polynucleotide sequence.

Optimal alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment method of Needleman and Wunsch (1970), by the search for similarity method of Pearson and
15 Lippman (1988), or the like. Computer implementations of the above algorithms are known as part of the Genetics Computer Group (GCG) Wisconsin Genetics Software Package (GAP, BESTFIT, BLASTA, FASTA and TFASTA), 575 Science Drive, Madison, WI. These programs are preferably run using default values for all parameters.

"Percentage of sequence identity" is determined by comparing two optimally
20 aligned sequences over a comparison window, wherein the portion of the sequence in the comparison window may comprise additions or deletions (*i.e.* "gaps") as compared to the reference sequence for optimal alignment of the two sequences being compared. The percentage identity is calculated by determining the number of positions at which the identical residue occurs in both sequences to yield the number of matched positions,
25 dividing the number of matched positions by the total number of positions in the window and multiplying the result by 100 to yield the percentage of sequence identity. Total identity is then determined as the average identity over all of the windows that cover the complete query sequence.

Fragments of Polypeptide

30 Genes which code for fragments of the full length polypeptides such as proteolytic cleavage fragments which contain at least one, and preferably all, of the above-listed physical and/or biological properties are also encompassed by the present invention.

DNA and RNA

The invention encompasses DNA that codes for any one of the above-described polypeptides including, but not limited to, those shown in SEQ ID NOS:2, 4, 6 and 21 including fusion polypeptides, variants and fragments thereof. The sequence of certain particularly useful cDNAs which encode polypeptides are shown in SEQ ID NOS:1, 3, 5 and 20. The present invention also includes cDNA as well as genomic DNA containing or comprising the requisite nucleotide sequences as well as corresponding RNA and antisense sequences.

Cloned DNA within the scope of the invention also includes allelic variants of the specific sequences presented in the attached Sequence Listing. An "allelic variant" is a sequence that is a variant from that of the exemplified nucleotide sequence, but represents the same chromosomal locus in the organism. In addition to those which occur by normal genetic variation in a population and perhaps fixed in the population by standard breeding methods, allelic variants can be produced by genetic engineering methods. A preferred allelic variant is one that is found in a naturally occurring organism, including a laboratory strain. Allelic variants are either silent or expressed. A silent allele is one that does not affect the phenotype of the organism. An expressed allele results in a detectable change in the phenotype of the trait represented by the locus.

A nucleic acid sequence "encodes" or "codes for" a polypeptide if it directs the expression of the polypeptide referred to. The nucleic acid can be DNA or RNA. Unless otherwise specified, a nucleic acid sequence that encodes a polypeptide includes the transcribed strand, the hnRNA and the spliced RNA or the DNA representative of the mRNA. An "antisense" nucleic acid is one that is complementary to all or part of a strand representative of mRNA, including untranslated portions thereof.

Degenerate Sequences

In accordance with degeneracy of genetic code, it is possible to substitute at least one base of the base sequence of a gene by another kind of base without causing the amino acid sequence of the polypeptide produced from the gene to be changed. Hence, the DNA of the present invention may also have any base sequence that has been changed by substitution in accordance with degeneracy of genetic code.

DNA Modification

The DNA is readily modified by substitution, deletion or insertion of nucleotides, thereby resulting in novel DNA sequences encoding the polypeptide or its derivatives.

These modified sequences are used to produce mutant polypeptide and to directly express the polypeptide. Methods for saturating a particular DNA sequence with random mutations and also for making specific site-directed mutations are known in the art; see *e.g.* Sambrook et al. (1989).

5 Hybridizable Variants

The DNA molecules useful in accordance with the present invention can comprise a nucleotide sequence selected from the group consisting of SEQ ID NOS.:1, 3, 5, 7-20 and 22-24 or can comprise a nucleotide sequence that hybridizes to a DNA molecule comprising the nucleotide sequence of SEQ ID NOS.:1, 3, 5 or 20 under salt and
10 temperature conditions providing stringency at least as high as that equivalent to 5x SSC and 42°C and that codes on expression for a polypeptide that has one or more or all of the above-described physical and/or biological properties. The present invention also includes polypeptides coded for by these hybridizable variants. The relationship of stringency to hybridization and wash conditions and other considerations of hybridization can be found
15 in Chapters 11 and 12 of Sambrook et al (1989). The present invention also encompasses functional promoters which hybridize to SEQ ID NOS:7, 8, 9 or 22 under the above-described conditions. DNA molecules of the invention will preferably hybridize to reference sequences under more stringent conditions allowing the degree of mismatch represented by the degrees of sequence identity enumerated above. The present invention
20 also encompasses functional primers or linker oligonucleotides set forth in SEQ ID NOS:10-19 and 23-24 or larger primers comprising these sequences, or sequences which hybridize with these sequences under the above-described conditions. The primers usually have a length of 10-50 nucleotides, preferably 15-35 nucleotides, more preferably 18-30 nucleotides.

25 Vectors

The invention is further directed to a replicable vector containing cDNA that codes for the polypeptide and that is capable of expressing the polypeptide.

The present invention is also directed to a vector comprising a replicable vector and a DNA sequence corresponding to the above described gene inserted into said vector. The
30 vector may be an integrating or non-integrating vector depending on its intended use and is conveniently a plasmid.

Transformed Cells

The invention further relates to a transformed cell or microorganism containing cDNA or a vector which codes for the polypeptide or a fragment or variant thereof and that

is capable of expressing the polypeptide.

Expression Systems Using Vertebrate Cells

Interest has been great in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of vertebrate host cell lines useful in the present invention preferably include cells from any of the fish described herein. Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located upstream from the gene to be expressed, along with a ribosome-binding site, RNA splice site (if intron-containing genomic DNA is used or if an intron is necessary to optimize expression of a cDNA), a polyadenylation site, and a transcription termination sequence.

EXAMPLES

The following examples are provided by way of illustration only and not by way of limitation. Those of skill will readily recognize a variety of noncritical parameters which can be changed or modified to yield essentially similar results.

15 **Example I: Isolation of skin-specific, muscle-specific and ubiquitously expressed zebrafish cDNA clones.**

cDNA clones were isolated and sequenced as described by Gong et al. (1997). Basically, random cDNA clones were selected from zebrafish embryonic and adult cDNA libraries and each clone was partially sequenced by a single sequencing reaction. The partial sequences were then used to identify the sequenced clones for potential function and tissue specificity. Of the distinct clones identified by this approach, four of them were selected: for skin specificity (clone A39 encoding cytokeratin, CK), for muscle specificity (clone E146 encoding muscle creatine kinase, MCK), for skeletal muscle specificity (clone A113 encoding the fast skeletal muscle isoform of the myosin light chain 2, MLC2f) and for ubiquitous expression (clone A150 encoding acidic ribosomal protein P0, ARP), respectively.

The four cDNA clones were sequenced, and their complete cDNA sequences with deduced amino acid sequences are shown in SEQ ID NOS:1, 3, 5, and 20 respectively. A39 encodes a type II basic cytokeratin and its closest homolog in mammals is cytokeratin 8 (65-68% amino acid identity). E146 codes for the zebrafish MCK and its amino acid sequence shares ~87% identity with mammalian MCKs. A113 encodes the fast skeletal muscle isoform of the myosin light chain 2. The deduced amino acid sequence of this gene is highly homologous to other vertebrate fast skeletal muscle MLC2f proteins (over 80%

amino acid identity). The amino acid sequence of zebrafish ARP deduced from the A150 clone is 87-89% identical to those of mammalian ARPs.

To demonstrate their expression patterns, whole mount *in situ* hybridization (Thisse et al., 1993) was performed for developing embryos and Northern blot analyses (Gong et al., 1992) were carried out for selected adult tissues and for developing embryos.

As indicated by whole mount *in situ* hybridization, cytokeratin mRNA was specifically expressed in the embryonic surface (Figs. 1A-1C) and cross section of *in situ* hybridized embryos confirmed that the expression was only in skin epithelia (Fig. 1C). Ontogenetically, the cytokeratin mRNA appeared before 4 hours post-fertilization (hpf) and it is likely that the transcription of the cytokeratin gene starts at mid-blastula transition when the zygotic genome is activated. By *in situ* hybridization, a clear cytokeratin mRNA signal was detected in highly flattened cells of the superficial layer in blastula and the expression remained in the superficial layer which eventually developed into skin epithelia including the yolk sac. In adult tissues, cytokeratin mRNA was predominantly detected in the skin and also weakly in several other tissues including the eye, gill, intestine and muscle, but not in the liver and ovary (Fig. 2). Therefore, the cytokeratin mRNA is predominantly, if not specifically, expressed in skin cells.

MCK mRNA was first detected in the first few anterior somites in 10 somite stage embryos (14 hpf) and at later stages the expression is specifically in skeletal muscle (Fig. 1D) and in heart (data not shown). When the stained embryos are cross-sectioned, the MCK mRNA signal was found exclusively in the trunk skeletal muscles (Fig. 1E). In adult tissues, MCK mRNA was detected exclusively in the skeletal muscle (Fig. 2).

MLC2f mRNA was specifically expressed in fast skeletal muscle in developing zebrafish embryos (Figs. 1H-1I). To examine the tissue distribution of MLC2f mRNA, total RNAs were prepared from several adult tissues including heart, brain, eyes, gills, intestine, liver, skeletal muscle, ovary, skin, and testis. MLC2f mRNA was only detected in the skeletal muscle by Northern analysis; while α -actin mRNA was detected ubiquitously in the same set of RNAs, confirming the validity of the assay (Fig. 2B).

ARP mRNA was expressed ubiquitously and it is presumably a maternal mRNA since it is present in the ovary as well as in embryos at one cell stage. In *in situ* hybridization experiments, an intense hybridization signal was detected in most tissues. An example of a hybridized embryo at 28 hpf is shown in Fig. 1F. In adults, ARP mRNA was abundantly expressed in all tissues examined except for the brain where a relatively weak signal was detected (Fig. 2A). These observations confirmed that the ARP mRNA is expressed ubiquitously.

Example II: Isolation of zebrafish gene promoters

Four zebrafish gene promoters were isolated by a linker-mediated PCR method as described by Liao *et al.*, (1997) and as exemplified by the diagrams in Fig. 3. The whole procedure includes the following steps: 1) designing of gene specific primers; 2) isolation of zebrafish genomic DNA; 3) digestion of genomic DNA by a restriction enzyme; 4) ligation of a short linker DNA to the digested genomic DNA; 5) PCR amplification of the promoter region; and 6) DNA sequencing to confirm the cloned DNA fragment. The following is the detailed description of these steps.

1. Designing of gene specific primers

Gene specific PCR primers were designed based on the 5' end of the four cDNA sequences and the regions used for designing the primers are shown in SEQ ID NOS: 1, 3, 5 and 20.

The two cytokeratin gene specific primers are:

CK1 (SEQ ID NO:10)

CK2 (SEQ ID NO:11), where the first six nucleotides are for creation of an EcoRI site to facilitate cloning.

The two muscle creatine kinase gene specific primers are:

MCK1 (SEQ ID NO:12), where the first five nucleotides are for creation of an EcoRI site to facilitate cloning.

MCK2 (SEQ ID NO:13), where the first three nucleotides are for creation of an EcoRI site to facilitate cloning.

The two fast skeletal muscle isoform of myosin light chain 2 gene specific primers are:

M1 (SEQ ID NO:23)

M2 (SEQ ID NO:24)

The two acidic ribosomal protein P0 gene specific primers are:

ARP1 (SEQ ID NO:14)

ARP2 (SEQ ID NO:15), where the first six nucleotides are for creation of an EcoRI site to facilitate cloning.

2. Isolation of zebrafish genomic DNA

Genomic DNA was isolated from a single individual fish by a standard method (Sambrook *et al.*, 1989). Generally, an adult fish was quickly frozen in liquid nitrogen and ground into powder. The ground tissue was then transferred to an extraction buffer (10 mM Tris, pH 8, 0.1 M EDTA, 20 µg/ml RNase A and 0.5% SDS) and incubated at 37°C for 1 hour. Proteinase K was added to a final concentration of 100 µg/ml and gently mixed until the mixture appeared viscous, followed by incubation at 50°C for 3 hours with periodical swirling. The genomic DNA was gently extracted three times by phenol equilibrated with Tris-HCl (pH 8), precipitated by adding 0.1 volume of 3 M NaOAc and 2.5 volumes of ethanol, and collected by swirling on a glass rod, then rinsed in 70% ethanol.

3. Digestion of genomic DNA by a restriction enzyme

Genomic DNA was digested with the selected restriction enzymes. Generally, 500 units of restriction enzyme were used to digest 50 µg of genomic DNA overnight at the optimal enzyme reaction temperature (usually at 37°C).

4. Ligation of a short linker DNA to the digested genomic DNA

The linker DNA was assembled by annealing equal moles of the two linker oligonucleotides, Oligo1 (SEQ ID NO:16) and Oligo 2 (SEQ ID NO:17). Oligo 2 was phosphorylated by T4 polynucleotide kinase prior to annealing. Restriction enzyme digested genomic DNA was filled-in or trimmed with T4 DNA polymerase, if necessary, and ligated with the linker DNA. Ligation was performed with 1 µg of digested genomic DNA and 0.5 µg of linker DNA in a 20 µl reaction containing 10 units of T4 DNA ligase at 4°C overnight.

5. PCR amplification of promoter region

PCR was performed with Advantage Tth Polymerase Mix (Clontech). The first round of PCR was performed using a linker specific primer L1 (SEQ ID NO:18) and a gene specific primer G1 (CK1, MCK1, M1 or ARP1). Each reaction (50 µl) contains 5 µl of 10x Tth PCR reaction buffer (1X= 15 mM KOAc, 40 mM Tris, pH 9.3), 2.2 µl of 25 mM Mg(OAc)₂, 5 µl of 2 mM dNTP, 1 µl of L1 (0.2 µg/µl), 1 µl of G1 (0.2 µg/µl), 33.8

µl of H₂O, and 1 µl (50 ng) of linker ligated genomic DNA and 1 µl of 50x Tth polymerase mix (Clontech). The cycling conditions were as follows: 94°C/1 min, 35 cycles of 94°C/30 sec and 68°C/6 min, and finally 68°C/8 min. After the primary round of PCR was completed, the products were diluted 100 fold. One µl of diluted PCR product was used as template for the second round of PCR (nested PCR) with a second linker specific primer L2 (SEQ ID NO:19) and a second gene specific primer G2 (CK2, MCK2, M2 or ARP2), as described for the primary PCR but with the following modification: 94°C/1 min, 25 cycles of 94°C/30 sec and 68°C/6 min, and finally 68°C/8 min. Both the primary and secondary PCR products were analyzed on a 1% agarose gel.

6. DNA sequencing to confirm the cloned DNA fragment

PCR products were purified from the agarose gel following electrophoresis and cloned into a TA vector, pT7Blue™ (Novogen). DNA sequencing was performed by dideoxynucleotide chain termination method using a T7 Sequencing Kit purchased from Pharmacia. Complete sequences of these promoter regions were obtained by automatic sequencing using a dRhodamine Terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer) and an ABI 377 automatic sequencing machine.

The isolated cyokeratin DNA fragment comprising the gene promoter is 2.2 kb. In the 3' proximal region immediately upstream of a portion identical to the 3' part of the CK cDNA sequence, there is a putative TATA box perfectly matching to a consensus TATA box sequence. The 164 bp of the 3' region is identical to the 5' UTR (untranslated region) of the cyokeratin cDNA. Thus, the isolated fragment was indeed derived from the same gene as the cyokeratin cDNA clone (SEQ ID NO:7). Similarly, a 1.5 kb 5' flanking region was isolated from the muscle creatine kinase gene, a putative TATA box was also found in its 3' proximal region and the 3' region is identical to the 5' portion of the MCK cDNA clone (SEQ ID NO:8). For MLC2f, a 2 kb region was isolated from the fast skeletal muscle isoform of myosin light chain 2 gene and sequenced completely. The promoter sequence for MLC2f is shown in SEQ ID NO:22. The sequence immediately upstream of the gene specific primer M2 is identical to the 5' UTR of the MLC2f cDNA clone; thus, the amplified DNA fragments are indeed derived from the MLC2f gene. A perfect TATA box was found 30 nucleotides upstream of the transcription start site, which was defined by a primer extension experiment based on Sambrook et al. (1989). In the 2-kb region comprising the promoter, six E-boxes (CANNTG) and six potential MEF2 binding sites [C/T)TA(T/A)4TA(A/G)] were found and are indicated in SEQ ID NO:22. Both of these cis-element classes are important for muscle specific gene transcription (Schwarz *et al.*, 1993; Olson *et al.*, 1995). A 2.2 kb fragment was amplified for the ARP gene. By

alignment of its sequence with the ARP cDNA clone, a 1.3 kb intron was found in the 5' UTR (SEQ ID NO:9). As a result, the isolated ARP promoter is within a DNA fragment about 0.8 kb long.

Example III: Generation of green fluorescent transgenic fish

5 The isolated zebrafish gene promoters were inserted into the plasmid pEGFP-1 (Clontech), which contains an EGFP structural gene whose codons have been optimized according to preferable human codons. Three promoter fragments were inserted into pEGFP-1 at the EcoRI and BamHI site and the resulting recombinant plasmids were named pCK-EGFP (Fig. 4), pMCK-EGFP (Fig. 5), and pARP-EGFP, respectively (Fig. 6). The
10 promoter fragment for the MLC2f gene was inserted into the Hind III and Bam HI sites of the plasmid pEGFP-1 and the resulting chimeric DNA construct, pMLC2f-EGFP, is diagramed in Fig. 7.

Linearized plasmid DNAs at a concentrations of 500 µg/ml (for pCK-EGFP and pMCK-EGFP) and 100 µg/ml (for pMLC2f-EGFP) in 0.1 M Tris-HCl (pH 7.6)/0.25%
15 phenol red were injected into the cytoplasm of 1- or 2-cell stage embryos. Because of a high mortality rate, pARP-EGFP was injected at a lower concentration (50 µg/ml). Each embryo received 300-500 pl of DNA. The injected embryos were reared in autoclaved Holtfreter's solution (0.35% NaCl, 0.01% KCl and 0.01% CaCl₂) supplemented with 1
20 µg/ml of methylene blue. Expression of GFP was observed and photographed under a ZEISS Axiovert 25 fluorescence microscope.

When zebrafish embryos received pCK-EGFP, GFP expression started about 4 hours after injection, which corresponds to the stage of ~30% epiboly. About 55% of the injected embryos expressed GFP at this stage. The early expression was always in the superficial layer of cells, mimicking endogenous expression of the CK gene as observed by
25 *in situ* hybridization. At later stages, in all GFP-expressing fish, GFP was found predominantly in skin epithelia. A typical pCK-EGFP transgenic zebrafish fry at 4 days old is shown in Fig. 8.

Under the MCK promoter, no GFP expression was observed in early embryos before muscle cells become differentiated. By 24 hpf, about 12% of surviving embryos
30 expressed GFP strongly in muscle cells and these GFP-positive embryos remain GFP-positive after hatching. The GFP expression was always found in many bundles of muscle fibers, mainly in the mid-trunk region and no expression was ever found in other types of cells. A typical pMCK-EGFP transgenic zebrafish fry (3 days old) is shown in Fig. 9.

Expression of pARP-EGFP was first observed 4 hours after injection at the 30%

epiboly stage. The timing of expression is similar to that of pCK-EGFP-injected embryos. However, unlike the pCK-EGFP transgenic embryos, the GFP expression under the ARP promoter occurred not only in the superficial layer of cells but also in deep layers of cells. In some batches of injected embryos, almost 100% of the injected embryos expressed initially. At later stages when some embryonic cells become overtly differentiated, it was found that the GFP expression occurred essentially in all different types of cells such as skin epithelia, muscle cells, lens, neural tissues, notochord, circulating blood cells and yolk cells (Fig. 10).

Under the MLC2f promoter, nearly 60% of the embryos expressed GFP. The earliest GFP expression started in trunk skeletal muscles about 19 hours after injection, which corresponds to the stage of 20-somite. Later, the GFP expression also occurred in head skeletal muscles including eye muscles, jaw muscles, gill muscles etc.

Transgenic founder zebrafish containing pMLC2f-EGFP emit a strong green fluorescent light under a blue or ultraviolet light (Fig. 11A). When the transgenic founders were crossed with wild-type fish, transgenic offspring were obtained that also displayed strong green fluorescence (Fig. 11B). The level of GFP expression is so high in the transgenic founders and offspring that green fluorescence can be observed when the fish are exposed to sunlight.

To identify the DNA elements conferring the strong promoter activity in skeletal muscles, deletion analysis of the 2-kb DNA fragment comprising the promoter was performed. Several deletion constructs, which contain 5' deletions of the MLC2f promoter upstream of the EGFP gene, were injected into the zebrafish embryos and the transient expression of GFP in early embryos (19-72 hpf) was compared. To facilitate the quantitative analysis of GFP expression, we define the level of expression as follows (Figs. 12A-12C):

Strong expression: GFP expression was detected in essentially 100% muscle fibers in the trunk.

Moderate expression: GFP expression was detected in several bundles of muscle fibers, usually in the mid-trunk region.

Weak expression: GFP expression occurred in dispersed muscle fibers and the number of GFP positive fibers is usually less than 20 per embryo.

As summarized in Fig. 13, deletion up to -283 bp maintained the GFP expression in skeletal muscles in 100% of the expressing embryos; however, the level of GFP expression from these deletion constructs varies greatly. Strong expression drops from

23% to 0% from the 2-kb (-2011 bp) promoter to the -283-bp promoter. Thus, only two constructs (-2011 bp and -1338 bp) are capable of maintaining the high level of expression and the highest expression was obtained only with the 2-kb promoter, indicating the importance of the promoter region of -1338 bp to -2011 bp for conferring the highest promoter activity.

The expression of GFP using pMLC2f-EGFP is much higher than that obtained using the pMCK-EGFP that contains a 1.5 kb of zebrafish *MCK* promoter. By the same assay in transient transgenic zebrafish embryos, only about 12% of the embryos injected with pMCK-EGFP expressed GFP. Among the expressing embryos, no strong expression was observed, and 70% and 30% showed moderate and weak expression, respectively. In comparison, about 60% of the embryos injected with pMLC2f-EGFP expressed GFP and 23%, 37% and 40% showed strong, moderate and weak expression, respectively.

Example IV: Potential applications of fluorescent transgenic fish

The fluorescent transgenic fish have use as ornamental fish in the market. Stably transgenic lines can be developed by breeding a GFP transgenic individual with a wild type fish or another transgenic fish. By isolation of more zebrafish gene promoters, such as eye-specific, bone-specific, tail-specific etc., and/or by classical breeding of these transgenic zebrafish, more varieties of fluorescent transgenic zebrafish can be produced. Previously, we have reported isolation of over 200 distinct zebrafish cDNA clones homologous to known genes (Gong et al., 1997). These isolated clones code for proteins in a variety of tissues and some of them are inducible by heat-shock, heavy metals, or hormones such as estrogens. By using the method of PCR amplification using gene-specific primers designed from the nucleotide sequences of these cDNAs, and the linker-specific primers described herein, the promoters of the genes represented by the cDNAs of Gong et al. can be used in the present invention. Thus, other tissue-specific promoters, hormone-inducible promoters, heavy-metal inducible promoters and the like from zebrafish can be isolated and used to make fluorescent zebrafish (or other fish species) that express a GFP or variant thereof, in response to the relevant compound.

Multiple color fluorescent fish may be generated by the same technique as blue fluorescent protein (BFP) gene, yellow fluorescent protein (YFP) gene and cyan fluorescent protein (CFP) gene are available from Clontech. For example, a transgenic fish with GFP under an eye-specific promoter, BFP under a skin-specific promoter, and YFP under a muscle-specific promoter will show the following multiple fluorescent colors: green eyes, blue skin and yellow muscle. By recombining different tissue specific promoters and fluorescent protein genes, more varieties of transgenic fish of different

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fluorescent color patterns will be created. By expression of two or more different fluorescent proteins in the same tissue, an intermediate color may be created. For example, expression of both GFP and BFP under a skin-specific promoter, a dark-green skin color may be created.

5 By using a heavy metal- (such as cadmium, cobalt, chromium) inducible or hormone- (such as estrogen, androgen or other steroid hormone) inducible promoter, a biosensor system may be developed for monitoring environmental pollution and for evaluating water quality for human consumption and aquacultural uses. In such a biosensor system, the transgenic fish will glow with a green fluorescence (or other color depending
10 on the fluorescence protein gene used) when pollutants such as heavy metals and estrogens (or their derivatives) reach a threshold concentration in an aquatic environment. Such a biosensor system has advantages over classical analytical methods because it is rapid, visualizable, and capable of identifying specific compounds directly in complex mixture found in an aquatic environment, and is portable or less instrument dependent. Moreover,
15 the biosensor system also provides direct information on biotoxicity and it is biodegradable and regenerative.

Environmental monitoring of several substances can be accomplished by either creating one transgenic fish having genes encoding different colored fluorescent proteins driven by promoters responsive to each substance. Then the particular colors exhibited the
20 fish in an environment can be observed. Alternatively, a number of fish can be transformed with individual vectors, then the fish can be combined into a population for monitoring an environment and the colors expressed by each fish observed.

In addition, the fluorescent transgenic fish should also be valuable in the market for scientific research tools because they can be used for embryonic studies such as tracing cell
25 lineage and cell migration. Cells from transgenic fish expressing GFP can also be used as cellular and genetic markers in cell transplantation and nuclear transplantation experiments.

The chimeric gene constructs demonstrated successfully in zebrafish in the present invention should also be applicable to other fish species such as medaka, goldfish, carp
30 including koi, loach, tilapia, glassfish, catfish, angel fish, discus, eel, tetra, goby, gourami, guppy, Xiphophorus (swordtail), hatchet fish, Molly fish, pangasius, etc. The promoters described herein can be used directly in these fish species. Alternatively, the homologous gene promoters from other fish species can be isolated by the method described in this invention. For example, the isolated and characterized zebrafish cDNA clones and
35 promoters described in this invention can be used as molecular probes to screen for homologous promoters in other fish species by molecular hybridization or by PCR.

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Alternatively, one can first isolate the zebrafish cDNA and promoters based on the sequences presented in SEQ ID NOS:1, 3, 5, 7, 8, 9, 20 and 22 or using data from other sequences of cDNAs disclosed by Gong et al. 1997, by PCR and then use the zebrafish gene fragments to obtain homologous genes from other fish species by the methods mentioned above.

In addition, a strong muscle-specific promoter such as MLC2f is valuable to direct a gene to be expressed in muscle tissues for generation of other beneficial transgenic fish. For example, transgenic expression of a growth hormone gene under the muscle-specific promoter may stimulate somatic growth of transgenic fish. Such DNA can be introduced either by microinjection, electroporation, or sperm carrier to generate germ-line transgenic fish, or by direct injection of naked DNA into skeletal muscles (Xu et al., 1999) or into other tissues or cavities, or by a biolistic method (gene bombardment or gene gun) (Gomez-Chiarri et al., 1996).

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SEQUENCE LISTING

<110> GONG, Zhiyuan
 LAM, Toong Jin
 JU, Bensheng
 XU, Yanfei
 — HE, Jiangyan
 YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT
 TRANSGENIC ORNAMENTAL FISH

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- 25 -

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Glu	Ala	Glu	Glu	Arg	Gly	Glu	Leu	Ala	Val	Lys	Asp	Ala	Lys	Leu	Arg		
				365				370						375			
atc	agg	gag	ctg	gag	gaa	gct	ctt	cag	agg	gcc	aag	caa	gac	atg	gcc	1265	
Ile	Arg	Glu	Leu	Glu	Glu	Ala	Leu	Gln	Arg	Ala	Lys	Gln	Asp	Met	Ala		
			380					385					390				
cgc	cag	gtc	cgc	gag	tac	cag	gag	ctc	atg	aac	gtc	aaa	ttg	gct	ctg	1313	
Arg	Gln	Val	Arg	Glu	Tyr	Gln	Glu	Leu	Met	Asn	Val	Lys	Leu	Ala	Leu		
		395				400					405						
gac	att	gag	atc	gcc	acc	tac	agg	aaa	ctg	ttg	gaa	gga	gag	gag	agc	1361	
Asp	Ile	Glu	Ile	Ala	Thr	Tyr	Arg	Lys	Leu	Leu	Glu	Gly	Glu	Glu	Ser		
	410					415					420						
aga	ctg	tcc	agc	ggt	gga	gct	caa	gct	acc	att	cat	gtt	cag	cag	acc	1409	
Arg	Leu	Ser	Ser	Gly	Gly	Ala	Gln	Ala	Thr	Ile	His	Val	Gln	Gln	Thr		
	425				430					435					440		
tcc	gga	ggt	gtt	tca	tct	ggt	tat	ggt	ggt	agc	ggc	tct	ggt	ttc	ggc	1457	
Ser	Gly	Gly	Val	Ser	Ser	Gly	Tyr	Gly	Gly	Ser	Gly	Ser	Gly	Phe	Gly		
				445				450						455			
tac	agc	agt	ggc	ttc	agc	agt	ggt	ggg	tca	gga	tac	ggt	agt	gga	tca	1505	
Tyr	Ser	Ser	Gly	Phe	Ser	Ser	Gly	Gly	Ser	Gly	Tyr	Gly	Ser	Gly	Ser		
			460					465						470			
gga	ttc	ggt	tct	gga	tca	ggg	tat	ggt	gga	ggc	tcc	atc	agc	aaa	acc	1553	
Gly	Phe	Gly	Ser	Gly	Ser	Gly	Tyr	Gly	Gly	Gly	Ser	Ile	Ser	Lys	Thr		
		475					480					485					
agt	gtc	acc	acc	gtc	agc	agt	aaa	cgc	tat	taa	ggagaagccc	gcccacaccc	1606				
Ser	Val	Thr	Thr	Val	Ser	Ser	Lys	Arg	Tyr								
490							495										
ccagccgaca	cagtttccaa	ccttccttac	ctgcaactag	atcccttctg	aaccttctta	1666											
cgactcaaac	catctatggt	gctatatatt	agccagacag	ctgtccctg	ttaatgagga	1726											
gatgtggacg	atgattttta	aagtacaaaa	taagtttttag	attgttctgt	gtgttgatgg	1786											
tagttacccg	tatcatgcat	ctcctgtctg	gtggtgtcac	tgcattttta	aatcatcaac	1846											
ccaactacac	taaaacgata	ccaggaagaa	tcgtgctcca	agccactgaa	tagtcttatt	1906											
tctgcactga	tatgtacagg	gaaagtgaga	cacatagaaa	ccactgtaac	ctacgtagta	1966											
ctatggtttc	actggatcag	gggtgtgcta	tacaagttcc	tgaatgtctt	gtttgaatgt	2026											
tttgtgctgt	tacaagctcc	ctgctgtagt	tttctgtgact	aatctgactt	ttgtcatttt	2086											
gctatggctg	tcagagttgg	tttacctatt	ttctataaaa	tgtatatggc	agtcagccaa	2146											
taactgatga	caattgcttg	tgggctacta	atgtccagtt	acctcacatt	caagggagat	2206											
ctgttacagc	aaaaaacagg	cacaatggga	tttatgtgga	ccatccctcc	ttaaccttgt	2266											

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gtactttccg tgttggaagt ggtgactgta ctgccttaca cattcccctg tattcaactg 2326
 gcttccagag catatatttac atccccggtt ataaatggaa aatgcaagaa aactgaaaca 2386
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 <213> Danio rerio

<400> 2

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 Gly Tyr Thr Ser Gln Ser Ala Tyr Ala Val Pro Ala Gly Ser Thr Arg
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 Met Ser Ser Val Thr Ser Val Arg Arg Ser Gly Val Gly Ala Ser Pro
 35 40 45
 Gly Phe Gly Ala Gly Gly Ser Tyr Ser Phe Ser Ser Ser Met Gly
 50 55 60
 Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly
 65 70 75 80
 Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Gln Asn Leu
 85 90 95
 Leu Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Gln Ala Val Arg
 100 105 110
 Thr Ser Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe
 115 120 125
 Leu Ile Asp Lys Val Arg Phe Leu Glu Gln Gln Asn Lys Met Leu Glu
 130 135 140
 Thr Lys Trp Ser Leu Leu Gln Glu Gln Thr Thr Thr Arg Ser Asn Ile
 145 150 155 160
 Asp Ala Met Phe Glu Ala Tyr Ile Ser Asn Leu Arg Arg Gln Leu Asp
 165 170 175
 Gly Leu Gly Asn Glu Lys Met Lys Leu Glu Gly Glu Leu Lys Asn Met
 180 185 190
 Gln Gly Leu Val Glu Asp Phe Lys Asn Lys Tyr Glu Asp Glu Ile Asn
 195 200 205
 Lys Arg Ala Ser Val Glu Asn Glu Phe Val Leu Leu Lys Lys Asp Val
 210 215 220
 Asp Ala Ala Tyr Met Asn Lys Val Glu Leu Glu Ala Lys Val Asp Ala
 225 230 235 240

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Leu	Gln	Asp	Glu	Ile	Asn	Phe	Leu	Arg	Ala	Val	Tyr	Glu	Ala	Glu	Leu
				245					250					255	
Arg	Glu	Leu	Gln	Ser	Gln	Ile	Lys	Asp	Thr	Ser	Val	Val	Val	Glu	Met
			260					265					270		
Asp	Asn	Ser	Arg	Asn	Leu	Asp	Met	Asp	Ser	Ile	Val	Ala	Glu	Val	Arg
		275					280					285			
Ala	Gln	Tyr	Glu	Asp	Ile	Ala	Asn	Arg	Ser	Arg	Ala	Glu	Ala	Glu	Ser
			290			295					300				
Trp	Tyr	Lys	Gln	Lys	Phe	Glu	Glu	Met	Gln	Ser	Thr	Ala	Gly	Gln	Tyr
305					310					315					320
Gly	Asp	Asp	Leu	Arg	Ser	Thr	Lys	Ala	Glu	Ile	Ala	Glu	Leu	Asn	Arg
				325					330					335	
Met	Ile	Ala	Arg	Leu	Gln	Asn	Glu	Ile	Asp	Ala	Val	Lys	Ala	Gln	Arg
			340					345					350		
Ala	Asn	Leu	Glu	Ala	Gln	Ile	Ala	Glu	Ala	Glu	Glu	Arg	Gly	Glu	Leu
			355				360					365			
Ala	Val	Lys	Asp	Ala	Lys	Leu	Arg	Ile	Arg	Glu	Leu	Glu	Glu	Ala	Leu
			370			375					380				
Gln	Arg	Ala	Lys	Gln	Asp	Met	Ala	Arg	Gln	Val	Arg	Glu	Tyr	Gln	Glu
385					390					395					400
Leu	Met	Asn	Val	Lys	Leu	Ala	Leu	Asp	Ile	Glu	Ile	Ala	Thr	Tyr	Arg
				405					410					415	
Lys	Leu	Leu	Glu	Gly	Glu	Glu	Ser	Arg	Leu	Ser	Ser	Gly	Gly	Ala	Gln
			420					425					430		
Ala	Thr	Ile	His	Val	Gln	Gln	Thr	Ser	Gly	Gly	Val	Ser	Ser	Gly	Tyr
			435				440					445			
Gly	Gly	Ser	Gly	Ser	Gly	Phe	Gly	Tyr	Ser	Ser	Gly	Phe	Ser	Ser	Gly
			450			455					460				
Gly	Ser	Gly	Tyr	Gly	Ser	Gly	Ser	Gly	Phe	Gly	Ser	Gly	Ser	Gly	Tyr
465					470				475						480
Gly	Gly	Gly	Ser	Ile	Ser	Lys	Thr	Ser	Val	Thr	Thr	Val	Ser	Ser	Lys
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Arg Tyr

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<222> (20)..(38)

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ttgtgcagtg	ttagaaaccg	caatc	atg	cct	ttc	gga	aac	acc	cac	aac	aac	112
			Met	Pro	Phe	Gly	Asn	Thr	His	Asn	Asn	
			1				5					

ttc	aag	ctg	aac	tac	tca	gtt	gat	gag	gag	tat	cca	gac	ctt	agc	aag	160
Phe	Lys	Leu	Asn	Tyr	Ser	Val	Asp	Glu	Glu	Tyr	Pro	Asp	Leu	Ser	Lys	
10					15					20					25	

cac	aac	aac	cac	atg	gcc	aag	gtg	ctg	act	aag	gaa	atg	tat	ggc	aag	208
His	Asn	Asn	His	Met	Ala	Lys	Val	Leu	Thr	Lys	Glu	Met	Tyr	Gly	Lys	
				30					35					40		

ctt	agg	gac	aag	cag	acc	cca	cct	gga	ttc	act	gtg	gat	gat	gtc	atc	256
Leu	Arg	Asp	Lys	Gln	Thr	Pro	Pro	Gly	Phe	Thr	Val	Asp	Asp	Val	Ile	
			45					50					55			

cag	act	ggt	gtt	gac	aat	cca	ggc	cac	ccc	ttc	atc	atg	acc	gtc	ggc	304
Gln	Thr	Gly	Val	Asp	Asn	Pro	Gly	His	Pro	Phe	Ile	Met	Thr	Val	Gly	
		60					65					70				

tgt	gtt	gct	ggt	gat	gag	gag	tcc	tac	gat	gtt	ttc	aag	gac	ctg	ttc	352
Cys	Val	Ala	Gly	Asp	Glu	Glu	Ser	Tyr	Asp	Val	Phe	Lys	Asp	Leu	Phe	
	75					80					85					

gac	ccc	gtc	att	tcc	gac	cgt	cac	ggt	gga	tac	aag	gca	act	gac	aag	400
Asp	Pro	Val	Ile	Ser	Asp	Arg	His	Gly	Gly	Tyr	Lys	Ala	Thr	Asp	Lys	
	90				95					100					105	

cac	aag	acc	gac	ctc	aac	ttt	gag	aac	ctg	aag	ggt	ggt	gat	gac	ctg	448
His	Lys	Thr	Asp	Leu	Asn	Phe	Glu	Asn	Leu	Lys	Gly	Gly	Asp	Asp	Leu	
				110					115					120		

gac	ccc	aac	tac	ttc	ctg	agc	agc	cgt	gtg	cgt	acc	gga	cgc	agc	atc	496
Asp	Pro	Asn	Tyr	Phe	Leu	Ser	Ser	Arg	Val	Arg	Thr	Gly	Arg	Ser	Ile	
			125					130					135			

aag	gga	tac	ccc	ctg	ccc	ccc	cac	aac	agc	cgt	gga	gag	cgc	aga	gct	544
Lys	Gly	Tyr	Pro	Leu	Pro	Pro	His	Asn	Ser	Arg	Gly	Glu	Arg	Arg	Ala	
		140					145					150				

gtg	gag	aag	ctg	tct	gtt	gaa	gct	ctg	agt	agc	ttg	gat	gga	gag	ttc	592
Val	Glu	Lys	Leu	Ser	Val	Glu	Ala	Leu	Ser	Ser	Leu	Asp	Gly	Glu	Phe	
	155					160					165					

aag	ggc	aag	tac	tac	ccc	ctg	aag	tcc	atg	act	gat	gac	gag	cag	gag	640
Lys	Gly	Lys	Tyr	Tyr	Pro	Leu	Lys	Ser	Met	Thr	Asp	Asp	Glu	Gln	Glu	
	170				175					180				185		

cag	ctg	atc	gct	gac	cac	ttc	ctc	ttt	gac	aaa	ccc	gtc	tcc	ccc	ctg	688
Gln	Leu	Ile	Ala	Asp	His	Phe	Leu	Phe	Asp	Lys	Pro	Val	Ser	Pro	Leu	
			190						195					200		

ctg	ctg	gct	gct	ggt	atg	gcc	cgt	gac	tgg	ccc	gat	gcc	aga	ggc	att	736
Leu	Leu	Ala	Ala	Gly	Met	Ala	Arg	Asp	Trp	Pro	Asp	Ala	Arg	Gly	Ile	

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205	210	215	
tgg cac aat gag aac aaa gcc ttc ctg gtc tgg gtg aaa cag gag gat			784
Trp His Asn Glu Asn Lys Ala Phe Leu Val Trp Val Lys Gln Glu Asp			
220	225	230	
—			
cac ctg cgt gtc att tcc atg cag aag ggt ggc aac atg aag gaa gtg			832
His Leu Arg Val Ile Ser Met Gln Lys Gly Gly Asn Met Lys Glu Val			
235	240	245	
ttc aag cgc ttc tgc gtt ggt ctt cag agg att gag gaa att ttc aag			880
Phe Lys Arg Phe Cys Val Gly Leu Gln Arg Ile Glu Glu Ile Phe Lys			
250	255	260	265
aag cac aac cat ggg ttc atg tgg aac gag cat ctt ggt ttc gtc ctg			928
Lys His Asn His Gly Phe Met Trp Asn Glu His Leu Gly Phe Val Leu			
270	275	280	
acc tgc ccc tcc aac ctg ggc aca ggc ctg cgc ggt gga gtc cac gtc			976
Thr Cys Pro Ser Asn Leu Gly Thr Gly Leu Arg Gly Gly Val His Val			
285	290	295	
aag ctg ccc aag ctc agc aca cat gcc aag ttt gag gag atc ctg acc			1024
Lys Leu Pro Lys Leu Ser Thr His Ala Lys Phe Glu Glu Ile Leu Thr			
300	305	310	
aga ctg cgc ctg cag aag cgt ggc aca ggg ggt gtg gac acc gct tcc			1072
Arg Leu Arg Leu Gln Lys Arg Gly Thr Gly Gly Val Asp Thr Ala Ser			
315	320	325	
gtt ggt gga gtg ttt gac att tcc aac gct gac cgt atc ggc tct tca			1120
Val Gly Gly Val Phe Asp Ile Ser Asn Ala Asp Arg Ile Gly Ser Ser			
330	335	340	345
gag gtt gag cag gtg cag tgt gtg gtt gat ggt gtc aag ctg atg gtg			1168
Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val			
350	355	360	
gag atg gag aag aag ctg gga gaa ggc cag tcc atc gac agc atg atc			1216
Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile			
365	370	375	
cct gcc cag aag taa agcgggaggc ccttccatctt ttttcttcgt ctttgtctgt			1271
Pro Ala Gln Lys			
380			
ttttttacag tccaacagca acgsagagga aaactgctgc tcaaaaagac agtctcacct			1331
ttgcacctgt cttcttttcc ttttttccct tcttctctaa tttccatgtc atttcgccat			1391
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<213> Danio rerio			
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Met Pro Phe Gly Asn Thr His Asn Asn Phe Lys Leu Asn Tyr Ser Val			

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Asp Glu Glu Tyr Pro Asp Leu Ser Lys His Asn Asn His Met Ala Lys	20	25	30
Val Leu Thr Lys Glu Met Tyr Gly Lys Leu Arg Asp Lys Gln Thr Pro	35	40	45
Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro	50	55	60
Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu	65	70	75
Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg	85	90	95
His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe	100	105	110
Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser	115	120	125
Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro	130	135	140
His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu	145	150	155
Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu	165	170	175
Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe	180	185	190
Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Leu Ala Ala Gly Met Ala	195	200	205
Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Glu Asn Lys Ala	210	215	220
Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met	225	230	235
Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly	245	250	255
Leu Gln Arg Ile Glu Glu Ile Phe Lys Lys His Asn His Gly Phe Met	260	265	270
Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly	275	280	285
Thr Gly Leu Arg Gly Gly Val His Val Lys Leu Pro Lys Leu Ser Thr	290	295	300
His Ala Lys Phe Glu Glu Ile Leu Thr Arg Leu Arg Leu Gln Lys Arg	305	310	315
Gly Thr Gly Gly Val Asp Thr Ala Ser Val Gly Gly Val Phe Asp Ile	325	330	335
Ser Asn Ala Asp Arg Ile Gly Ser Ser Glu Val Glu Gln Val Gln Cys	340	345	350

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Val Val Asp Gly Val Lys Leu Met Val Glu Met Glu Lys Lys Leu Gly
 355 360 365

Glu Gly Gln Ser Ile Asp Ser Met Ile Pro Ala Gln Lys
 370 375 380

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<211> 1104

<212> DNA

<213> Danio rerio

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<223> ARP2

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<223> ARP1

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gaagcactgc aaag atg ccc agg gaa gac agg gcc acg tgg aag tcc aac 110
 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn
 1 5 10

tat ttt ctg aaa atc atc caa ctg ctg gat gac ttc ccc aag tgt ttc 158
 Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe
 15 20 25

atc gtg ggc gca gac aat gtc ggc tcc aag cag atg cag acc atc cgt 206
 Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg
 30 35 40

ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg 254
 Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met
 45 50 55 60

atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag 302
 Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu
 65 70 75

agg ctg ctt ccc cac atc cgc ggg aac gtg ggc ttc gtc ttc acc aag 350
 Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys
 80 85 90

gag gat ctg act gag gtc cga gac ctg ctg ctg gca aac aaa gtg ccc 398
 Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
 95 100 105

gct gct gcc cgt gct ggt gcc atc gcc ccc tgt gag gtg act gtg ccg 446
 Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro
 110 115 120

gcc cag aac acc ggg ctc ggt cct gag aag acc tct ttc ttc cag gct 494

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Ala	Gln	Asn	Thr	Gly	Leu	Gly	Pro	Glu	Lys	Thr	Ser	Phe	Phe	Gln	Ala		
125					130					135					140		
ttg	gga	atc	acc	acc	aag	atc	tcc	aga	gga	acc	att	gaa	atc	ttg	agt	542	
Leu	Gly	Ile	Thr	Thr	Lys	Ile	Ser	Arg	Gly	Thr	Ile	Glu	Ile	Leu	Ser		
—				145					150					155			
gac	gtt	cag	ctt	atc	aaa	cct	gga	gac	aag	gtg	ggc	gcc	agc	gag	gcc	590	
Asp	Val	Gln	Leu	Ile	Lys	Pro	Gly	Asp	Lys	Val	Gly	Ala	Ser	Glu	Ala		
			160					165					170				
acg	ctg	ctg	aac	atg	ctg	aac	atg	ctg	aac	atc	tcg	ccc	ttc	tcc	tac	638	
Thr	Leu	Leu	Asn	Met	Leu	Asn	Met	Leu	Asn	Ile	Ser	Pro	Phe	Ser	Tyr		
			175				180					185					
ggg	ctg	atc	atc	cag	cag	gtg	tat	gat	aac	ggc	agt	gtc	tac	agc	ccc	686	
Gly	Leu	Ile	Ile	Gln	Gln	Val	Tyr	Asp	Asn	Gly	Ser	Val	Tyr	Ser	Pro		
	190					195					200						
gag	gtg	ctg	gac	atc	act	gag	gac	gcc	ctg	cac	aag	agg	ttc	ctg	aag	734	
Glu	Val	Leu	Asp	Ile	Thr	Glu	Asp	Ala	Leu	His	Lys	Arg	Phe	Leu	Lys		
	205				210					215					220		
ggt	gtg	agg	aac	atc	gcc	agt	gtg	tgt	ctg	cag	atc	ggc	tac	cca	act	782	
Gly	Val	Arg	Asn	Ile	Ala	Ser	Val	Cys	Leu	Gln	Ile	Gly	Tyr	Pro	Thr		
			225					230						235			
ctt	gct	tcc	atc	cct	cac	act	atc	atc	aat	gga	tac	aag	agg	gtc	ctg	830	
Leu	Ala	Ser	Ile	Pro	His	Thr	Ile	Ile	Asn	Gly	Tyr	Lys	Arg	Val	Leu		
			240					245					250				
gct	gtc	act	gtc	gaa	aca	gac	tac	aca	ttc	ccc	ttg	gct	gag	aag	gtg	878	
Ala	Val	Thr	Val	Glu	Thr	Asp	Tyr	Thr	Phe	Pro	Leu	Ala	Glu	Lys	Val		
			255				260					265					
aag	gcc	tac	ctg	gct	gat	ccc	acc	gct	ttc	gct	gtt	gca	gcc	cct	gtt	926	
Lys	Ala	Tyr	Leu	Ala	Asp	Pro	Thr	Ala	Phe	Ala	Val	Ala	Ala	Pro	Val		
			270			275					280						
gcg	gca	gct	aca	gag	cag	aaa	tcc	gct	gct	cct	gcg	gct	aaa	gag	gag	974	
Ala	Ala	Ala	Thr	Glu	Gln	Lys	Ser	Ala	Ala	Pro	Ala	Ala	Lys	Glu	Glu		
	285				290					295					300		
gca	ccc	aag	gag	gat	tct	gag	gag	tct	gat	gaa	gac	atg	ggc	ttc	ggc	1022	
Ala	Pro	Lys	Glu	Asp	Ser	Glu	Glu	Ser	Asp	Glu	Asp	Met	Gly	Phe	Gly		
				305				310					315				
ctg	ttt	gat	taa	accagacacc	gaatatccat	gtctgttttaa	catcaataaa									1074	
Leu	Phe	Asp															
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Met	Pro	Arg	Glu	Asp	Arg	Ala	Thr	Trp	Lys	Ser	Asn	Tyr	Phe	Leu	Lys		
1				5					10					15			
Ile	Ile	Gln	Leu	Leu	Asp	Asp	Phe	Pro	Lys	Cys	Phe	Ile	Val	Gly	Ala		
			20					25					30				

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Asp	Asn	Val	Gly	Ser	Lys	Gln	Met	Gln	Thr	Ile	Arg	Leu	Ser	Leu	Arg
		35					40					45			
Gly	Lys	Ala	Val	Val	Leu	Met	Gly	Lys	Asn	Thr	Met	Met	Arg	Lys	Ala
	50					55					60				
Ile	Arg	Gly	His	Leu	Glu	Asn	Asn	Pro	Ala	Leu	Glu	Arg	Leu	Leu	Pro
	65				70					75					80
His	Ile	Arg	Gly	Asn	Val	Gly	Phe	Val	Phe	Thr	Lys	Glu	Asp	Leu	Thr
				85					90					95	
Glu	Val	Arg	Asp	Leu	Leu	Leu	Ala	Asn	Lys	Val	Pro	Ala	Ala	Ala	Arg
			100					105					110		
Ala	Gly	Ala	Ile	Ala	Pro	Cys	Glu	Val	Thr	Val	Pro	Ala	Gln	Asn	Thr
		115					120					125			
Gly	Leu	Gly	Pro	Glu	Lys	Thr	Ser	Phe	Phe	Gln	Ala	Leu	Gly	Ile	Thr
	130					135					140				
Thr	Lys	Ile	Ser	Arg	Gly	Thr	Ile	Glu	Ile	Leu	Ser	Asp	Val	Gln	Leu
	145				150					155					160
Ile	Lys	Pro	Gly	Asp	Lys	Val	Gly	Ala	Ser	Glu	Ala	Thr	Leu	Leu	Asn
				165					170					175	
Met	Leu	Asn	Met	Leu	Asn	Ile	Ser	Pro	Phe	Ser	Tyr	Gly	Leu	Ile	Ile
			180					185					190		
Gln	Gln	Val	Tyr	Asp	Asn	Gly	Ser	Val	Tyr	Ser	Pro	Glu	Val	Leu	Asp
		195					200					205			
Ile	Thr	Glu	Asp	Ala	Leu	His	Lys	Arg	Phe	Leu	Lys	Gly	Val	Arg	Asn
	210					215					220				
Ile	Ala	Ser	Val	Cys	Leu	Gln	Ile	Gly	Tyr	Pro	Thr	Leu	Ala	Ser	Ile
	225				230					235					240
Pro	His	Thr	Ile	Ile	Asn	Gly	Tyr	Lys	Arg	Val	Leu	Ala	Val	Thr	Val
				245					250					255	
Glu	Thr	Asp	Tyr	Thr	Phe	Pro	Leu	Ala	Glu	Lys	Val	Lys	Ala	Tyr	Leu
			260					265					270		
Ala	Asp	Pro	Thr	Ala	Phe	Ala	Val	Ala	Ala	Pro	Val	Ala	Ala	Ala	Thr
		275					280					285			
Glu	Gln	Lys	Ser	Ala	Ala	Pro	Ala	Ala	Lys	Glu	Glu	Ala	Pro	Lys	Glu
	290					295					300				
Asp	Ser	Glu	Glu	Ser	Asp	Glu	Asp	Met	Gly	Phe	Gly	Leu	Phe	Asp	
	305				310					315					

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<210> 7
<211> 2241
<212> DNA
<213> Danio rerio

<220>
<221> TATA_signal
<222> (2103)..(2108)
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<220>
<221> primer_bind
<222> (2221)..(2241)
<223> CK2

<220>
<221> misc_feature
<222> (2142)..(2235)
<223> Identical to the 5' CK cDNA

<400> 7
ccttcccttc tacttttgac gtccttttaa gagcttgtgc atgaaagcag atttggagct 60
gattactcat ctcaaacacc catacaaagg gatgattgcc gtaccatgat ctcacacctt 120
tcacacctgg ttatactat gatagtgtga gacgattgcg taatgctatt aaatgcccat 180
cagtgtctggc tgtgacaccc aactgctgcc atttcgtgtt gacttgcacg agaaatgaga 240
aattgtctga ctatgcaggg tgtctatgcg tgggaacatt tatcagtggc cattaaatac 300
tatagtttac agttagacca aagtgtgctg tatttttgtg ttagcttagc tgcagttttt 360
gtgtgtgaag taacaaatga caaatactca aactattgta attaagtagt ttttctcaga 420
aattgtaatt tactaagtag tttaaaaatg tgtactttta ctttcccttg agtacatttt 480
tagtgcagtg ttggtacttt tatttcactt ctttccctca acctgcagtc actactttat 540
ttattcttgt ctatgtggat tagacaaatc agtcctgtga ttctgtcca atcaaattgc 600
acatagaagg taaatcacat cataatgaac taccttaaga catgggccat ttataattgc 660
agcaaactgt ttgccagcat taaaagaaga tgtcaaaaat atttacacgc attaaccag 720
agactgctta gatgcatgtc actgatgaga agatgatgga tgtttactgt atgatgaccg 780
aaataacttt aaacgcacac aagacggcac aagacgtcaa catggcgcta ggttgacgtt 840
gtaccccaac gcagtgggga cgttgcattt tgtttagaaa tgaaaattag gttgacgtca 900
gaactcaacg tcaggtcgat gtcaatgttc aacatccaat ctaaaatcat atatcaatgt 960
ctaattgatgt tacagcttga tgttatgcgg atgttacccc tatgacgtct atcagacgtt 1020
ggattatggt tgccatacct gatgaataaa tgtcattatt tgacgttggt ttaagatgtt 1080
ggttcgacat tggattttgg tcgctttcca acacaacctt aatccacca atattaactt 1140
cctatgacat cgttattgga cgtcaaaata acaatatect tagatgctgg ctgacttttg 1200
aatttaggtc accacaacct atatttaacc taatattaac atcttatgat gttgtgtgcc 1260
tgctgggcaa taactaaatg cactacagaa tgttacgttt acacacatgt aaattacatg 1320
taaattgcac agcttttcac agcataatac tcactactta ctactcttga gtacttttaa 1380
aaaagctact tttcactcat actttgagta atatttaca ctgatacttt tactcgcaact 1440
acatttttag gcatgtattg atatttttac tatgattttt cagtactctt tccactactg 1500
cagccctccc catacataat cgtatgttta cacatatggt ggagttttag gccataatct 1560
acattagctt tgtagccgc tagcattact gtgcagaatt gtgtgtgtgc acattttcca 1620

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atatcaatac agaaggaaac tgtgttccct gttcccttgt aaatctcaac aatgcaactg 1680
 ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaaag tgaatggaaa 1740
 aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa gagcagaggt 1800
 taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca caccgctgg 1860
 cagatggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtctcaagt 1920
 ctcaagcctc tcttgctt ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
 caacatttat cttaccactt tctctctgta cctgtctaac aggtagggtg tgtgtgagag 2040
 tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccacct ctcaagagt 2100
 tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctccttg 2160
 tgagcaacct cctccactca ctctctctc agagagcact ctctacctc cttctcagca 2220
 actcaaagac acaggatccg g 2241

<210> 8
 <211> 1456
 <212> DNA
 <213> Danio rerio

<220>
 <221> TATA signal
 <222> (1389)..(1394)

<220>
 <221> primer_bind
 <222> (1433)..(1456)
 <223> MCK2

<220>
 <221> misc_feature
 <222> (1428)..(1453)
 <223> Identical to the 5' MCK cDNA

<400> 8
 gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
 tgtggcttaa tcttggtga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
 gcatgtgcac catgacaggc ctgttattca cacttggtgc catgttgag actgttcggc 180
 cagctatagt tttcttcaca gagtctggg tcacctaatg tcacaaggaa gaaacatgtt 240
 acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
 ttacagctta aaagattgct agacagaaaa accagggagg ggttttccca taatatccag 360
 tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
 gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc ttaaaagaag 480
 acacaacagg gatagttcac ccaaaaaaca gaccattctt ttttctgtt gaacaaaaat 540
 taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
 aagtcaatgg gtcttccagc attttttcaa tataccttac tttagattca aaagaaaaac 660

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acatctcaaa taggtttgag gttgaataaa cttttttcat tttggggtgg actatcccta 720
 attatttgac acttaagatt tatagtaa at ctttttatag actttctccc cttattaaac 780
 atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccctg 840
 tcaa atggtt ttgtgtatgg ttggcgcaca atagactgaa ctggcctatc acacagactt 900
 tcataacaac tccagttgat gccctttcac cctcagtgtg taaatatggc gtctgacatg 960
 agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagtttgac 1020
 ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggcctgacac 1080
 ggcgacttct gatattctgtg gtatgtttgg caaaagtgtc gctcagcctt tttagcatgg 1140
 cagatcctcc acatcccatc acccctcctt caacctattc cctcctggaa agctatgtat 1200
 ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260
 catctaggat gcctggggcc taaattgaag cttttcttac actaaacagg gcataagaga 1320
 ccagcgccag ccaatcataa ttcagtgagc tctaaaatgg gccagccaat ggctgcaggg 1380
 gctagaggta tatatatcca aatcaaaactc ttcttgcttg ggtgaccctt atttcggctt 1440
 ggtgaacagg atccgg 1456

<210> 9
 <211> 2205
 <212> DNA
 <213> Danio rerio

<220>
 <221> primer_bind
 <222> (2179)..(2205)
 <223> ARP2

<220>
 <221> misc_feature
 <222> (2153)..(2199)
 <223> Identical to the 5' ARP cDNA

<220>
 <221> intron
 <222> (792)..(2152)

<220>
 <221> misc_feature
 <222> (775)..(791)
 <223> Identical to the 5' ARP cDNA

<400> 9
 atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgac 60
 attttaattt gtgttgata attttacatt ttgtaagtat tatttttata aaaaatatat 120
 agaaataata caaatttggt tacagtattc ttagttattg caataaacga attttatata 180
 gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
 tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
 agataataaa gtgacttttt tgggcggacc aaatttcctt attaatggtc aattcattaa 360

aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagattt ttggctgttg ttagaagggg tacatctgcg gccgaaagt aacgggaact 480
attt~~a~~cattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatgc 600
tatattgacc gcagctgtat cttttctaag tgcgactgta caaatacgcg ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgcaca gatacgcatt ttccgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctctttct ttcacgcgtc 780
cctaccgtga ggtaaggctg acgccgctct tgtggcggtt tcttaaaatg tgtaataaaa 840
taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900
tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgtagca 960
caggcctcgt gcgccatgtg tgacgcgacg ttttaatagc atcttatttg attttgatga 1020
tccgattctg atattaatca ttttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080
ttacatgcta gtacttgtgc tagtcggctg atccacattg agatgttgcg ctatttgcca 1140
ttttaaaacc agttactctc attttagtga aatattctta agccactaag ttaaaatttg 1200
tcaatcacat ataattgtgt ttatgtttta tttagatcat cataccaggt aatagtttta 1260
tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
gtaaagttaa tcttaaaggg gtaaaggctc acccaaaaga caattcaccg tcaagtgttt 1380
tcaaattctta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560
tgcataaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620
gcagtggtca ccaagcttgt tcctgaaggg ccagtgtcct acagatttta gctccaaccc 1680
taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740
gcaggtgtgt tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800
gtgacccttg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860
ttatggacag gctgttgca gcttgttcg tcgttccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcagggg cgctgggtctc agacacgttt 1980
atagcagtaa atcaaataca atagtgtctt gattatcttt aaatatttga aagcttataa 2040
taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaat 2100
aagatgcaca caaggcaggt gtaaaagtat tgcttgtgtt tgtaatcctc agattttaca 2160
accttgtctt taaaccggct gttcacgat ccttggaagg gatcc 2205

<210> 10

<211> 24

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
— gene specific primer

<400> 10
cgctggagta agagatagac ctgg

24

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
gene specific primer

<220>
<221> misc_feature
<222> (1)..(6)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 11
ccggatcctg tgtctttgag ttgctg

26

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 12
ccggatcctt gggatcagat cctg

24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (1)..(3)
<223> Introduced for restriction site

<220>
<221> misc_feature

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<222> (3)..(8)
<223> BamHI site

<400> 13
ccggatcctg ttcaccaagc cgaa 24

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc 25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<220>
<221> misc_feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI site

<400> 15
ggatcccttc caaggatcgg tgaaca 26

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<400> 16
gttcattctt acaagctagc gctgaacaat gctgtggaca agcttgaatt c 51

<210> 17
<211> 10

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

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<220>

<223> n is a dideoxycytidine

<400> 17

gaattcaagn

10

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker
specific primer

<400> 18

gttcattcttt acaagctagc g

21

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker
specific primer

<400> 19

tcctgaacaa tgctgtggac

20

<210> 20

<211> 1392

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (42)..(551)

<220>

<221> primer_bind

<222> (6)..(28)

<223> M2

<220>

<221> primer_bind

<222> (23)..(45)

<223> M1

<220>

<221> polyA_signal

<222> (797)..(802)

<220>

<221> polyA_signal

<222> (1351)..(1357)

<400> 20

ctcttcttga tcttcttaga cttcacacat accgtctcga c atg gca ccc aag aag 56

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Met Ala Pro Lys Lys
1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104
Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser
10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152
Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile
25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200
Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asn Leu Arg Asp
40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248
Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu
55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296
Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
70 75 80 85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344
Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile
90 95 100

gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392
Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys
105 110 115

aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440
Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr
120 125 130

gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488
Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala
135 140 145

ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536
Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu
150 155 160 165

gag aag gag gag taa acaaccttgg aatcaagaaa acgaagagaa gaacatgcat 591
Glu Lys Glu Glu
170

cctcacagct taatctccag tctgttgtct ggccttctct aacttttggt tttccttct 651

ccctttcttg ctttctacca tcgttggttac tccaagcact tacactctcc atcttaccaa 711

agacttgtct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771

cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt 831

ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag 891

cttgcatgta agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta 951

tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga 1011

aagaagcacg atggagtgat ctcaactctat aatagaggaa ccagtcatca ttctcatttc 1071

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ctcctctggt ggttgactaa aaagagaaag agaaaatgag ggttttgtgc tgagtgagtt 1131
tagcctccta aaagcgatgc cgagctcatc acagagggag tgagagggac agaccatcct 1191
aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccct 1251
cctcttctct atttctctgt ccattctttt tttttctttt tttctttttt gctttctgca 1311
tctgggcctg ctttgctctg ccaaacctct cctgtaacca ataaaaagac acaaactgtg 1371
aataaaaaaa aaaaaaaaaa a 1392

<210> 21
<211> 169
<212> PRT
<213> Danio rerio

<400> 21
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
1 5 10 15
Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
20 25 30
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
35 40 45
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
50 55 60
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
65 70 75 80
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
85 90 95
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
100 105 110
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
115 120 125
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
130 135 140
Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
145 150 155 160
Ile Thr His Gly Glu Glu Lys Glu Glu
165

<210> 22
<211> 2054
<212> DNA
<213> Danio rerio

<220>
<221> TATA_signal
<222> (1983)..(1989)

<220>
<221> enhancer
<222> (142)..(148)

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<223> E-box, canntg

<220>

<221> enhancer

<222> (452)..(457)

<223> E-box, canntg

<220>

<221> enhancer

<222> (1095)..(1100)

<223> E-box, canntg

<220>

<221> enhancer

<222> (1278)..(1283)

<223> E-box, canntg

<220>

<221> enhancer

<222> (1362)..(1367)

<223> E-box, canntg

<220>

<221> enhancer

<222> (1385)..(1390)

<223> E-box, canntg

<220>

<221> enhancer

<222> (523)..(532)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<221> enhancer

<222> (606)..(615)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<221> enhancer

<222> (697)..(706)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<221> enhancer

<222> (1490)..(1499)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<221> enhancer

<222> (1640)..(1649)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<221> enhancer

<222> (1956)..(1965)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<223> Transcription start site at residue 2012

<220>

<221> primer_bind

<222> (2032)..(2054)

<223> M2

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<220>

<221> misc_difference

<222> (2027)..(2054)

<223> Identical to the 5' MLC2f cDNA

<400> 22

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<223> Description of Artificial Sequence: MLC2F gene
specific primer M2

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23

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CLAIMS

1. A zebrafish cytokeratin gene promoter which is capable of directing a structural gene to be predominantly expressed in skin epithelia when it is inserted in front of the structural gene and introduced into fish embryos.
2. A zebrafish muscle creatine kinase gene promoter which is capable of directing a structural gene to be specifically expressed in muscles when it is inserted in front of the structural gene and introduced into fish embryos.
3. A zebrafish fast skeletal muscle isoform of myosin light chain 2 gene promoter which is capable of directing a structural gene to be predominantly expressed in skeletal muscles when it is inserted in front of the structural gene and introduced into fish embryos.
4. A zebrafish acidic ribosomal protein P0 gene promoter which is capable of directing a structural gene to be expressed ubiquitously in all tissues when it is inserted in front of the structural gene and introduced into fish embryos.
5. A recombinant DNA molecule comprising a structural gene and the promoter of claim 1, 2, 3 or 4 arranged upstream of said structural gene.
6. A chimeric gene comprising the promoter of claim 1, 2, 3 or 4, operatively linked to DNA encoding a protein selected from the group consisting of GFP, modified GFP, EGFP, BFP, EBFP, YFP, EYFP, CFP, ECFP, luciferase, β -galactosidase, chloramphenicol acetyltransferase, and growth hormone.
7. A transgenic fish comprising a chimeric gene comprising the promoter of claim 1, 2, 3 or 4.
8. The transgenic fish of claim 7, which contains said promoter in germ cells and/or in somatic cells and which is capable of breeding with either a said transgenic fish or a non-transgenic fish to produce viable and fertile transgenic progeny.
9. The transgenic fish of claim 7, and progeny of said fish that emits green fluorescence when the whole fish is exposed to a blue or ultraviolet light.
10. A transgenic fish comprising a DNA that encodes a fluorescent protein under control of a promoter that causes said DNA (1) to be expressed in predominately

skin epithelia, (2) to be specifically expressed in muscles, (3) to be predominantly expressed in skeletal muscles, or (4) to be expressed ubiquitously in all tissues.

— 11. The transgenic fish of claim 8, wherein said fluorescent protein is expressed a level sufficient that said fish fluoresces upon exposure to sunlight or daylight.

5 12. The transgenic fish of claim 11, wherein said high expression is induced by exposure of said fish to a steroid compound or to a heavy metal.

13. The transgenic fish of claim 10, wherein said promoter is a promoter which naturally occurs in the genome of a fish of the same species as the transgenic fish.

10 14. A recombinant DNA vector comprising a promoter DNA that hybridizes under stringent conditions to a polynucleotide of any one of SEQ ID NOS:7, 8, 9, or 22, operatively linked to a structural gene encoding a fluorescent or chemiluminescent protein.

15. A cell transformed with the vector of claim 14.

15 16. A transgenic fish comprising a chimeric gene in turn comprising a promoter DNA that hybridizes under stringent conditions to a polynucleotide of any one of SEQ ID NOS:7, 8, 9, or 22, operatively linked to a structural gene encoding a fluorescent or a chemiluminescent protein.

17. A method for sensing a steroid hormone or a steroid hormone derivative in a water sample comprising:

20 (a) contacting a fish expressing a fluorescent or chemiluminescent protein under control of an estrogen- or other steroid hormone-inducible promoter with a sample of water; and

(b) measuring the amount of fluorescent or chemiluminescent light from said fish.

25 18. A method for sensing heavy metals, such as zinc, copper, cadmium, mercury etc., in a water sample comprising:

(a) contacting a fish expressing a fluorescent or chemiluminescent protein under control of a heavy metal-inducible promoter with a sample of water; and

(b) measuring the amount of fluorescent or chemiluminescent light from said fish.

Fig. 1A

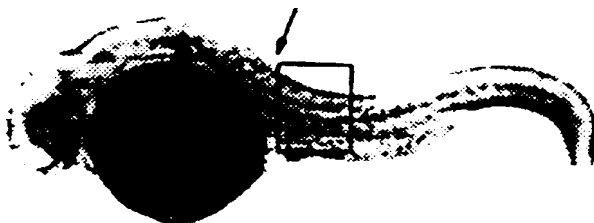


Fig. 1B

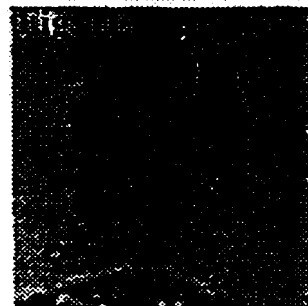
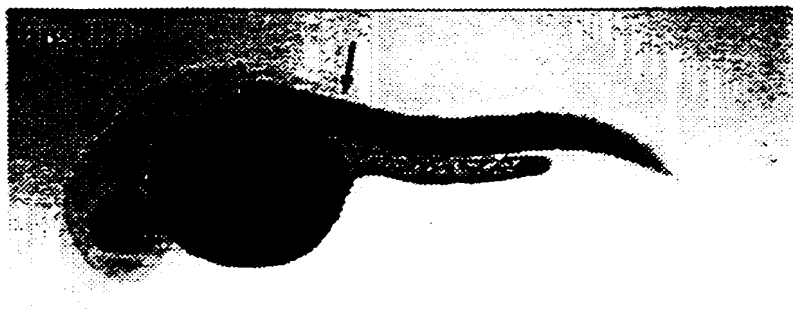
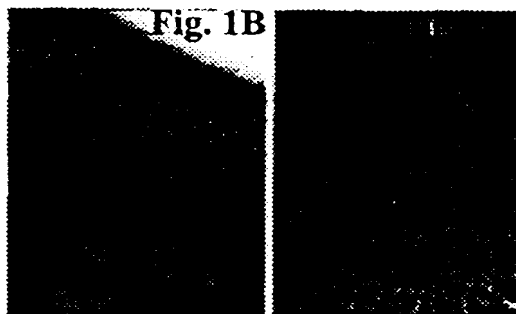




Fig. 1H



Fig. 1I

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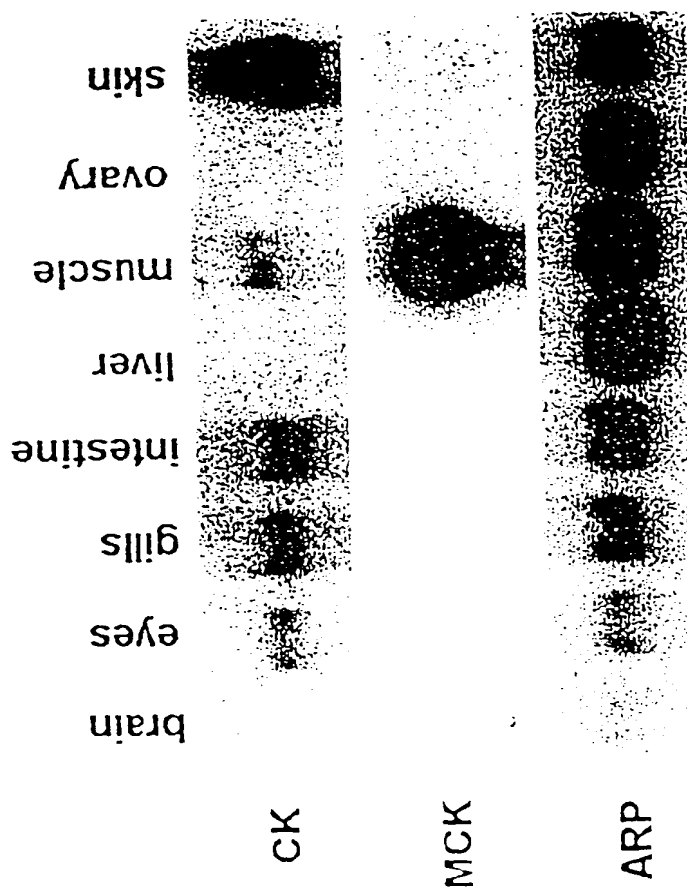


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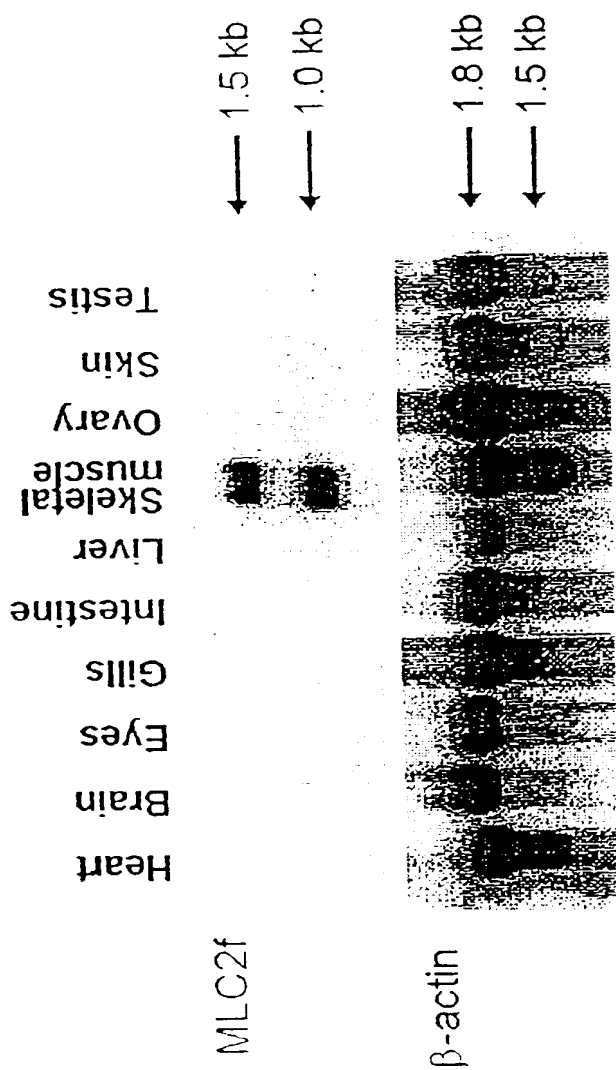


Fig. 2B

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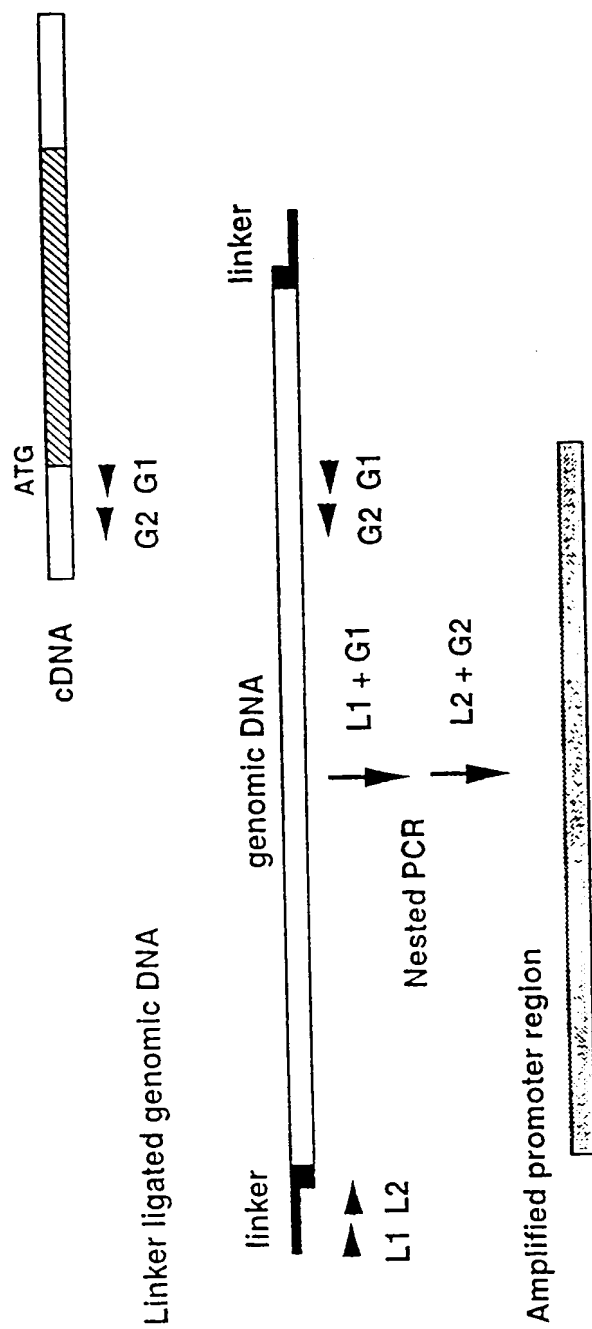


Fig. 3

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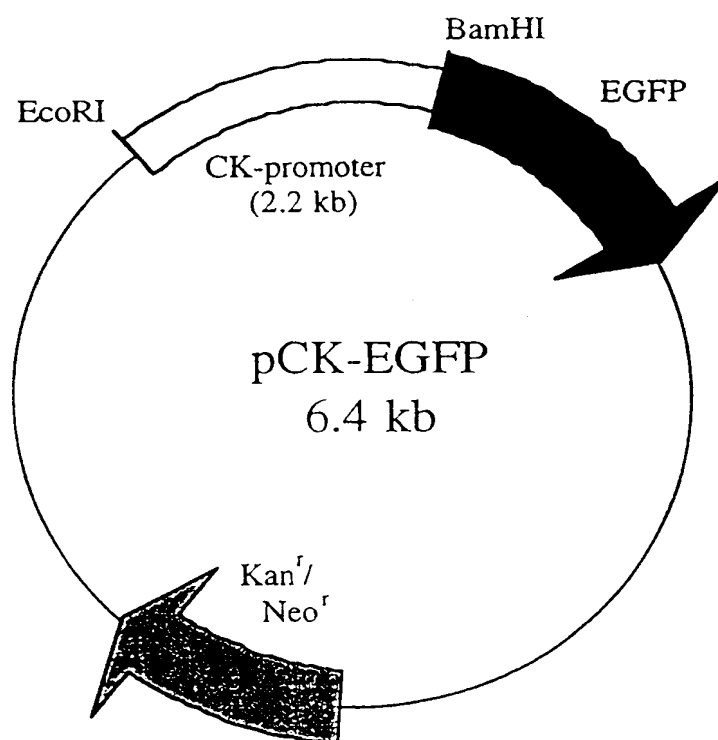


Fig. 4

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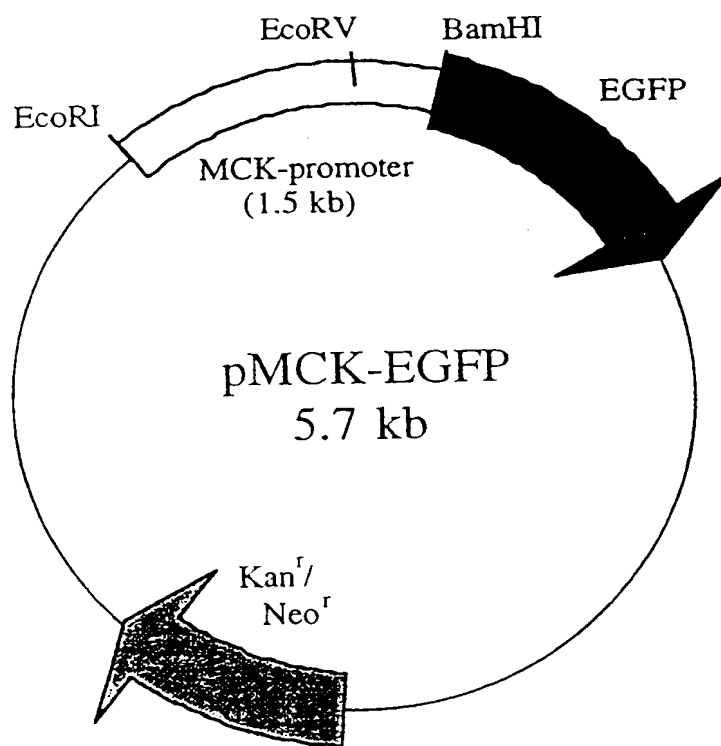


Fig. 5

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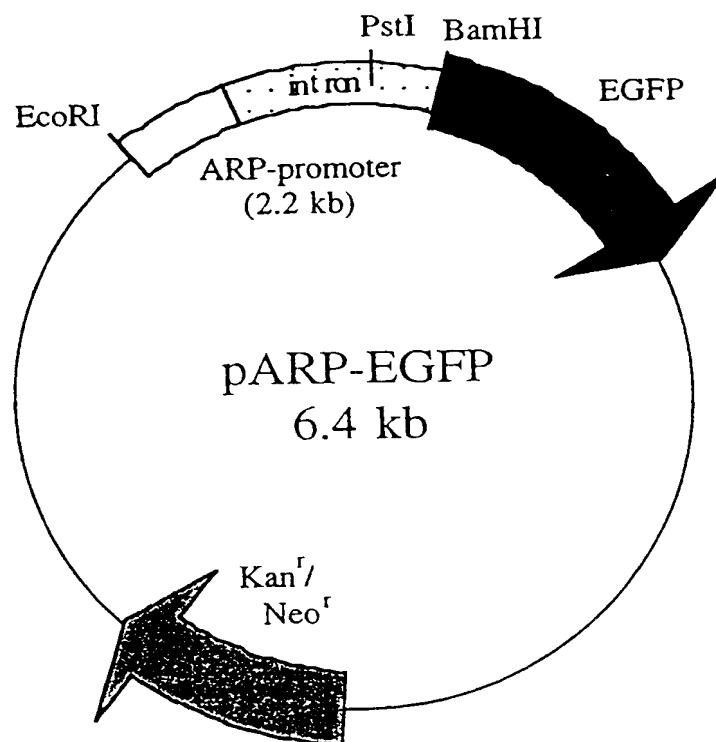


Fig. 6

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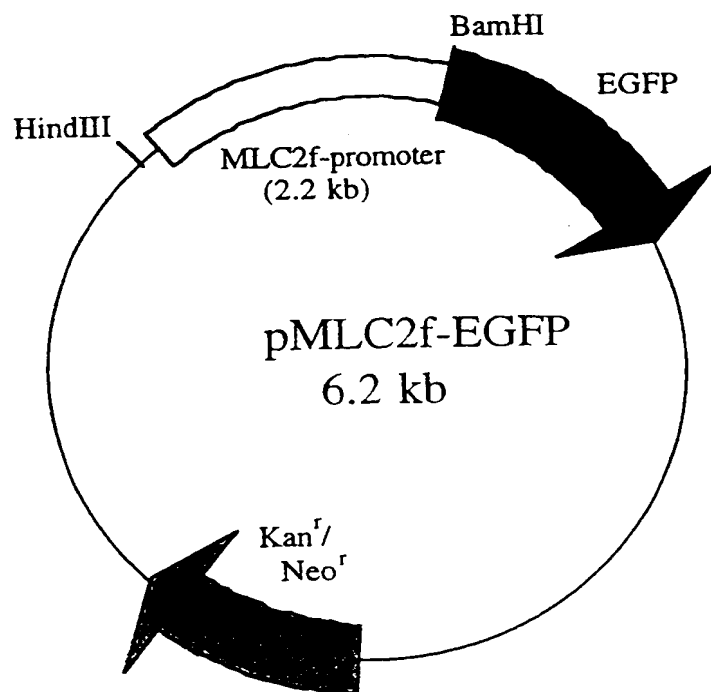


Fig. 7

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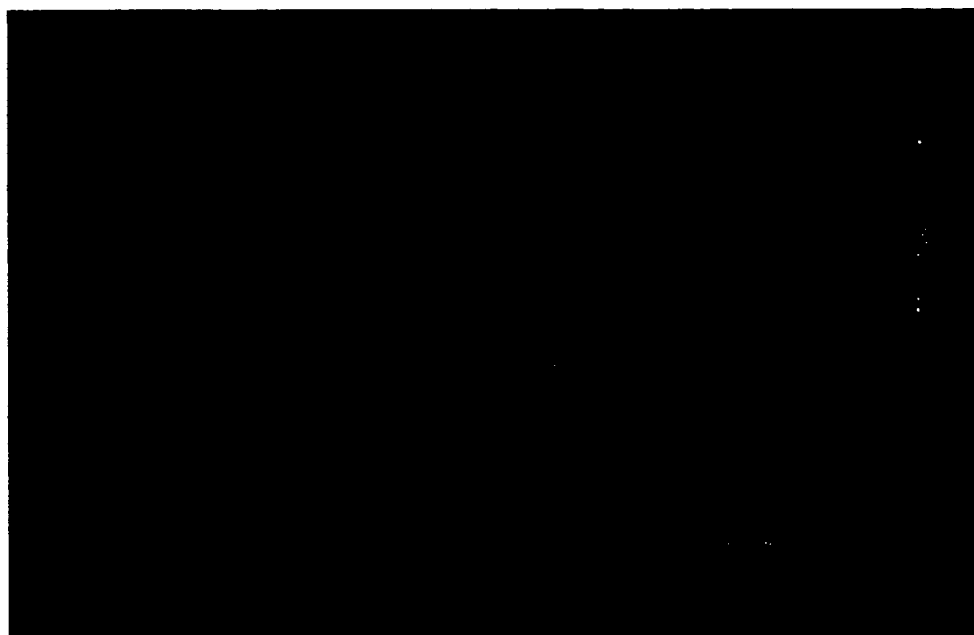


Fig. 8

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Fig. 9

- 12/15 -

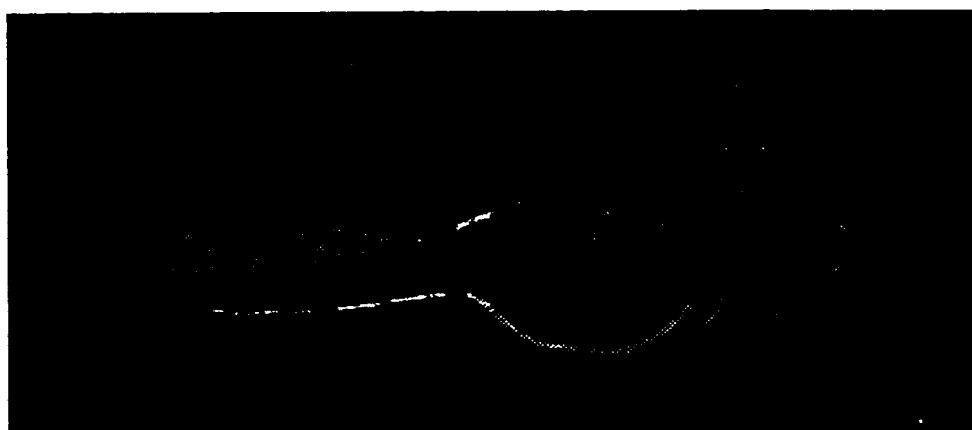


Fig. 10



Fig. 11A



Fig. 11B

- 14/15 -

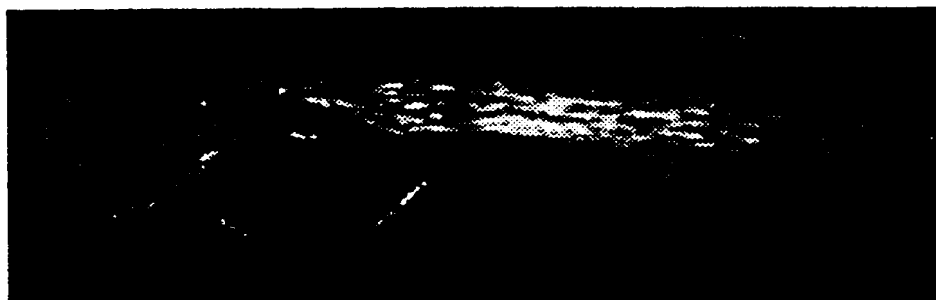


Fig. 12A

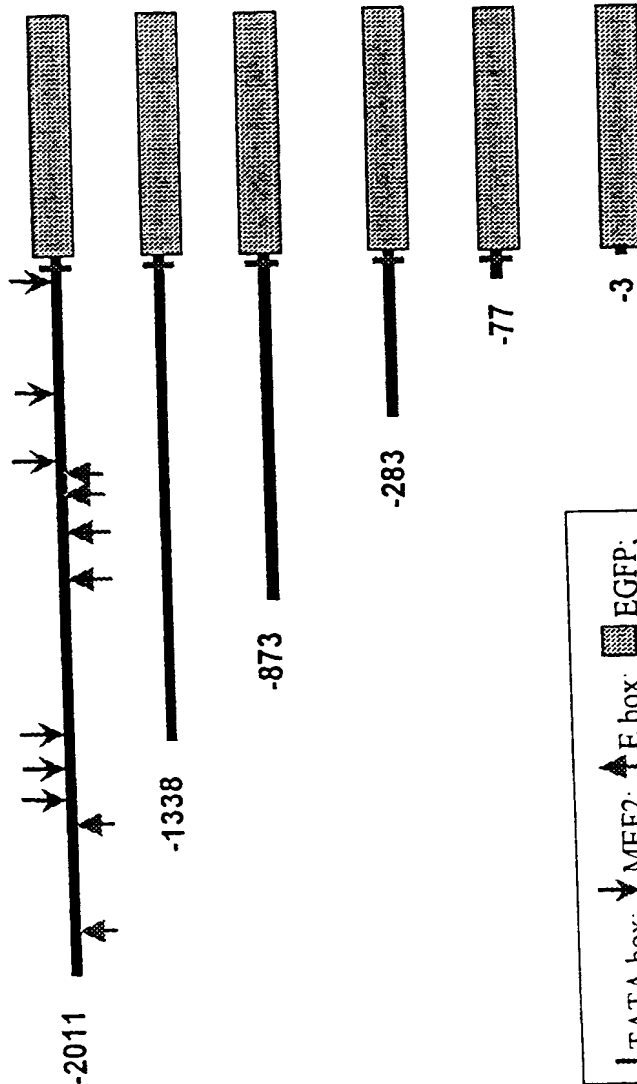


Fig. 12B



Fig. 12C

Fig. 13



Exp. in skeletal muscles (%)	Levels of Exp. in Skeletal muscles (%)		
	S	M	W
100	23	37	40
100	14	23	63
100	2	30	68
100	0	15	85
95.7	0	11	89
46.6	0	0	100

S, Strong Expression; M, Medial Expression; W, Weak Expression

INTERNATIONAL SEARCH REPORT

International application No.
PCT/SG 99/00079

A. CLASSIFICATION OF SUBJECT MATTER

IPC⁷: C 12 N 15/12, 5/16; C 12 Q 1/66, 1/48

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC⁷: C 12 N 15/12, 5/16; C 12 Q 1/66, 1/48

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WPI, PAJ, CAS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 98/56902 A2 (MEDICAL COLLEGE OF GEORGIA RESEARCH INSTITUTE, INC.) 17 December 1998 (12.12.98) abstract; claims 1-9, 19, 20, 25-30.	1-8, 13-18
A	WO 96/03034 A1 (MASSACHUSETTS INSTITUTE OF TECHNOLOGY) 08 February 1996 (08.02.96) page 2; claims 1, 2, 9, 10, 29-35.	1-8, 14-16
A	WO 9815627 A1 (UNIVERSITY OF SOUTHAMPTON) 16 April 1998 (16.04.98) claims 1, 2, 5, 6, 11-14, 20-29.	1-8
A	MULLER et al. "Activator effect of coinjected enhancers on the muscle-specific expression of promoters of zebrafish embryos" Mol. Reprod. Dec. 1997, 47(4), 404-412 (Eng). Chem. abstr. Vol. 127, No. 10, 08 September 1997 (08.09.97) (Columbus, Ohio, USA) page 195, right column, the abstract No. 131871y ----	2,3,5-7

☐ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents:

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„O“ document referring to an oral disclosure, use, exhibition or other means

„P“ document published prior to the international filing date but later than the priority date claimed

„T“ later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

„X“ document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

„Y“ document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

„&“ document member of the same patent family

Date of the actual completion of the international search

12 November 1999 (12.11.99)

Date of mailing of the international search report

13 December 1999 (13.12.99)

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Mosser

Telephone No. 1/53424/437

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/SG 99/00079

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